SEARCH REQUEST FORM

Requestor's Name:		Serial Number:	
Date:	Phone:	Ar	t Unit:
terms that may have a special	meaning. Give examples or n	specifically as possible the subject elevent citations, authors, keywor py of the broadest and/or most rel	t matter to be searched. Define any ds, etc., if known. For sequences, event claim(s).
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Date completed: 08-	28.03	Search Site	Vendors
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Terminal time: 2 d	 .	Pre-S	Dialog
CPU time:		Type of Search	APS
Total time: Number of Searches:	25	N.A. Sequence A.A. Sequence	Geninfo SDC
Number of Databases:	2	Structure	DARC/Questel
		Bibliographic	Other CGN

PTO-1590 (9-90)

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Page 1

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Minimum
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Maximum Match 100%
Listing first 45 summaries
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DB seq length: 2000000000
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August 28, 2003, 14:10:52; Search time 376 Seconds (without alignments) 30.092 Million cell updates/sec
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/ Cgn2_6/ptodata/1/paa/US093_COMB.pep: *
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/ Cgn2_6/ptodata/1/paa/US098_COMB.pep: *
/ Cgn2_6/ptodata/1/paa/US101_COMB.pep: *
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Result No.

Score				ID	Descr
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ALIGNMENTS

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CURRENT APPLICATION UNMER: US/09/845,738A
CURRENT FILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 1
SOPTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR F.
TITLE OF INVENTION: OF 1562 DALTONS
FILE REFERENCE: 2132.040
                                                                                   Query Match
Best Local S
                                                                    Matches
                                                                                     Local Similarity
ITHRIHWESASLL 13
                              ITHRIHWESASLL 13
                                                                    Conservative
                                                                                 100.0%; Score 70; DB 23; 100.0%; Pred. No. 0.00025;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-349A-1
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GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR TITLE OF INVENTION: OF 1690 DALTONS
FILE REFERENCE: 2132.042
CURRENT APPLICATION NUMBER: US/09/845,730
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS 1
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
SEQ ID NO 1
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Best Local Similarity 100.
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Best Local Similarity
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APPLICANT: Marshall, John
APPLICANT: Thatcher, Brad
TITLE OF INVENTION: Biopolymer Marker Indicative Of Disease State Having A Molecular
TITLE OF INVENTION: of 1449 Daltons
TITLE OF INVENTION UNBERG: US/09/846,349A
CURRENT APPLICATION NUMBERG: US/09/846,349A
CURRENT FILING DATE: 2001-04-30
SEQ ID NO 1
                           APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 1777 DALTONS
FILE REFERENCE: 2132.043
CURRENT APPLICATION NUMBER: US/09/845,735
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
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                SOFTWARE: PatentIn version 3.1
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Pred. No. 0.00027
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Pred. No. 0.00027;
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RESULT 7
US-09-846-345-1
; Sequence 1, Application US/09846345
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-735-1
                                                                                                                                                                                                                                                            ; TYPE: PRT; ORGANISM: Homo sapiens US-09-845-730A-1
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SEQ ID NO 1
LENGTH: 15
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GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR V
TITLE OF INVENTION: OF 1793 DALTONS
FILE REFERENCE: 2132.044
CURRENT APPLICATION NUMBER: US/09/845,739
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 2132.042
CURRENT APPLICATION NUMBER: US/09/845,730A
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09845730A
GENERAL INFORMATION:
APPLICANT: Jackowski, George
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Best Local Similarity
APPLICANT: Jackowski, George
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR TITLE OF INVENTION: OF 1690 DALTONS
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                                                                                                                                                                                                                                                                                                               LENGTH: 16
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Pred. No. 0.00029;
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Pred. No. 0.00031;
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CURRENT APPLICATION NUMBER: US/09/846,345
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-09-846-345-1
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US-09-846-344-1
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US-09-846-344-1
                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09846345A GENERAL INFORMATION: APPLICANT: Jackowski, George
                                                                                        Query Match
                                                                                                                                                                                                 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 13; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09846344 GENERAL INFORMATION:
                                                      Matches
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Best Local
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TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 2021 DALTONS
FILE REFERENCE: 2132.048
CURRENT APPLICATION NUMBER: US/09/846,344
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR TITLE OF INVENTION: OF 1865 DALTONS FILE REFERENCE: 2132.045 CURRENT APPLICATION NUMBER: US/09/846,345A CURRENT FILING DATE: 2001-04-30
                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR TITLE OF INVENTION: OF 1865 DALTONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 2132.045
                                                                                                                               LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
                                                                       Local
                                                    l Similarity
13; Conserv
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ITHRIHWESASLL 13
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                                                      Conservative
                                                                   100.0%;
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                                              Score 70; DB 23;
Pred. No. 0.00033;
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Pred. No. 0.00033;
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                                                                                    Length 17;
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RESULT 12
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; ORGANISM: Homo sapiens
US-09-846-346-1
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FURRENT APPLICATION NUMBER: US/09/846,346
CURRENT APPLICATION NUMBER: US/09/846,346
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEO ID NOS: 1
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
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; GENERAL INFORMATION:
; APPLICANT: Ladunga,
; APPLICANT: Spier, E
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LENGTH: 18
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GENERAL INFORMATION
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Best Local :
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Best Local Similarity
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TITLE OF INVENTION: Biopolymer Marker Indicative Of Disease State Having A Molecular 1
TITLE OF INVENTION: 0f 1998 Daltons
FILE REFERENCE: 2132.013
CURRENT APPLICATION NUMBER: US/09/846,346A
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOPTWARE: Patentin version 3.1
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TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 1998 DALTONS
APPLICANT: Dubman, Alex
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
                                       APPLICANT:
APPLICANT:
                                                                                           APPLICANT:
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APPLICANT: Marshall, John
APPLICANT: Yantha, Jason
APPLICANT: Vrees, Tammy
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                         Greenberg, Simon
                                                                                                                             Ladunga, Steven Istvan
                                                        Wang, Yu
                                                                      Brandenberger, Ralph
                                                                                                                                                                  Application US/60242679
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Pred. No.
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CURRENT APPLICATION UNMBER: US/60/242,679
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 2265
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 943
LENGTH: 677
TYPE: PRT
ORGANISM: HUMAN
US-60-242-679-943
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US-09-724-676A-66913
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66913
LENGTH: 770
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SEQ ID NO 66913
LENGTH: 770
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Best Local Similarity
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Best Local :
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 0.012;
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Pred. No. 0.011;
; Mismatches
                                                                      Score 70; DB 21;
Pred. No. 0.012;
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Sequence 66911, Application US/09724676

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 66911

LENGTH: 785

TYPE: PRT
                                                                                                               Sequence 66914, Application US/09724676

GENERAL INFORMATION:
APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 66914

LENGTH: 733
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US-09-724-676-66911
                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-66914
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US-09-724-676-66914
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US-09-724-676A-66911
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GENERAL INFORMATION:
GENERAL INFORMATION: USACIANTS OF Alternative splicing
TITLE OF INVENTION: Variants of alternative splicing
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 66911
LENGTH: 785
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Best Local (
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 Best Local Similarity
Matches 13; Conserva
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mes 13; Conservative
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Score 70; DB 21
Pred. No. 0.013;
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Pred. No. 0.012;
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ITHRIHWESASLL 13

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Sequence 66904, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
FILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 66904
LENCTH: 804
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US-09-724-676A-66904
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US-09-724-676-66904
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US-09-724-676A-66914
; ORGANISM: Homo sapiens
US-09-724-676A-66904
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US-09-724-676-66904
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APPLICANT: Compugen LTD
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 793
TYPE: PRT
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SOPTWARE: Patentin version 3.2
SEQ ID NO 66904
LENGTH: 804
TYPE: PRT
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Best Local Similarity
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Similarity 100.0%;
13; Conservative 0
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Pred. No. 0.013;
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Pred. No. 0.013;
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RESULT 23
US-09-724-676-66908
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US-09-724-676-66907
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Sequence 66908, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 66907, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 66907
LENGTH: 812
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nes 13; Conservative
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Sequence 66912, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66912
LENGTH: 830
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676-66912
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TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66908
LENGTH: 822
TYPE: PRT
 RESULT 26
US-09-724-676A-66912
; Sequence 66912, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternal
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; ORGANISM: Homo sapiens
US-09-724-676-66908
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US-09-724-676-66912
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US-09-724-676A-66908
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LENGTH: 822
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Local Similarity 100.0%;
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Pred. No. 0.013;
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Pred. No. 0.013;
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Sequence 66902, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 66902
LENGTH: 841
TYPE: PRT
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US-09-724-676-66902
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US-09-724-676A-66902
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CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: BatentIn version 3.2
SEQ ID NO 66912
LENGTH: 830
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 66902
LENGTH: 841
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
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Best Local Similarity
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                                                                              Similarity
ITHRIHWESASLL 483
                                                                Conservative
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                                                                            100.0%; Score 70; DB 21; Length 841; 100.0%; Pred. No. 0.013;
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100.0%; Pred. No.
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RESULT 29

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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 66905
LENGTH: 849
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-66905
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US-09-724-676A-66905
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US-09-724-676-66909
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US-09-724-676-66905
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66909
LENGTH: 850
                                Matches
                                            Query Match
Best Local
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GENERAL INFORMATION:
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Best Local
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GENERAL INFORMATION:
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GENERAL INFORMATION
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
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SOFTWARE: PatentIn version 3.2
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TYPE: PRT
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Local Similarity 100.0%;
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                                            Score 70; DB 21;
Pred. No. 0.013;
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Pred. No. 0.013;
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                                                          Length 850;
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RESULT 34
US-09-724-676A-66903
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US-09-724-676A-66909
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US-09-724-676-66903
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                                    APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 66903
LENGTH: 869
TLENGTH: 869
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66903
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CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66909
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Best Local Similarity
Matches 13; Conserv
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ORGANISM: Homo sapiens
09-724-676A-66903
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TYPE: PRT
                                  TYPE: PRT
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ORGANISM: Homo sapiens
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Pred. No.
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Pred. No.
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CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 66906
LENGTH: 876
TYPE: PRT
ORGANISM: Homo sapiens.
US-09-724-676A-66906
                                                RESULT 37

US-09-724-676-66876

Sequence 66876, Application US/09724676

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Cusyon

CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222
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US-09-724-676A-66906
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66906
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CIUDENEM ADDITION: VALUE COMPUSED COMPANY VALUE COMPUSED COMPANY VALUE COMPUSED COMPUSED COMPANY VALUE C
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Best Local
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Best Local
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SEQ ID
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TYPE: PRT
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   NO 66876
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Similarity 100.0%;
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                         PatentIn version 3.2
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US-09-724-676A-66876
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RESULT 40
US-09-724-676A-66880
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                                                                                                                                                                                                                                             Sequence 66880, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
RUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66876
LENGTH: 1190
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Pred. No. 0.019;
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Sequence 66880, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen

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CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 66880

LENGTH: 1198

TYPE: PRT

ORGANISM: Homo sapiens

US-09-724-676A-66880

Query Match
Best Local Similarity 100.0%; Score 70; DB 21; Length 1198;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Seps 0;

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Db 876 ITHRIHWESASLL 888

Search completed: August 28, 2003, 14:21:19

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16.625 Million cell updates/sec
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        US-10-379-747-2
US-10-408-765A-3010
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US-10-613-520-1720
US-09-319-724B-19
US-09-319-724B-1
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US-10-624-932-26
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PCT-US03-06859-2
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Sequence 14, Appl
Sequence 15, Appl
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	67, Appl		26, Appl	6891, Ap	1213, Ap	797, App	21, Appl	778, App	6253, Ap	1551, Ap	205, App		•	6463, Ap	•	15056, A	927, App	2327, Ap	Jan 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

ALIGNMENTS

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APPLICATION CUMBER: 607365,420
PRIOR PILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 60/365,420
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PRIOR APPLICATION NUMBER: 60/365,420
PRIOR FILING DATE: 2002-03-15
PRIOR PILING DATE: 2002-03-15
PRIOR PILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 60/365,420
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PRIOR PILING DATE: 2002-03-15
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PRIOR PILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 60/365,477
PRIOR APPLICATION NUMBER: 60/365,477
PRIOR PILING DATE: 2002-03-19
SOFTWARE: CuraSeqList version 0.1
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LENGTH: 705
TYPE: PRT
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CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-09-845-738C-1
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application PC/TUS0306859 GENERAL INFORMATION:
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APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE
TITLE OF INVENTION: OF 1562 DALTONS
FILE REFERENCE: 2132.040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ITHRIHWESASLL 13
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13; Conserv
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
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; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 705
; TYPE: PRT
; ORGANLEM: Homo sapiens
US-10-379-747-4
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US-10-379-747-4
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PCT-US03-06859-2
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PCT-US03-06859-4
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 70; DB 6; Best Local Similarity 100.0%; Pred. No. 0.00033; Matches 13; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/365,034
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 60/365,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                           APPLICANT: Curagen Corporation, et al TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOR FILE REFERENCE: 21402-5688-061 CURRENT APPLICATION NUMBER: PCT/US03/06859 CURRENT FILING DATE: 2003-03-06 CURRENT FILING DATE: 2003-03-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/366,420 PRIOR FILING DATE: 2002-03-21 PRIOR APPLICATION NUMBER: 60/365,477 PRIOR FILING DATE: 2002-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rastelli, Luca ;
APPLICANT: Rieger, Daniel K.;
APPLICANT: Shimkets, Richard A.;
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
                                                                    PRIOR APPLICATION NUMBER: 10/379,747
PRIOR FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: 60/365,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/379,747
CURRENT FILING DATE: 2003-03-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 21402-568B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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APPLICATION NUMBER: 60/365,477
               APPLICATION NUMBER: 60/366,420 FILING DATE: 2002-03-21
                                                    FILING DATE:
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13; Conserv
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Gangolli, Esha A.;
Malyankar, Uriel M.;
Miller, Charles E.;
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Patturajan, Meera;
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                                                  2002-03-15
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Pred. No. 0.00033;
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RESULT 5
US-10-379-747-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-06859-2
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                                                                                                                 US-09-897-516A-4590
                                                                                                                               RESULT 6
                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-10-379-747-2
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Best Local Similarity
Matches 13; Conserv
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NUMBER OF SEQ ID NOS: 45
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 2
                                                                                 Sequence 4590, Application US/09897516A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2
                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                            Query Match
                                                 APPLICANT: Corbin, David R. APPLICANT: Goldman, Barry
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/365,034
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 60/366,420
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/365,477
PRIOR FILING DATE: 2002-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 21402-568B
CURRENT APPLICATION NUMBER: US/10/379,747
CURRENT FILING DATE: 2003-03-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Burgess,
                                                                                                                                                                                                                                                                                                                                              LENGTH: 16
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shimkets, Richard A.;
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                              Local
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13; Conserv
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Hinkle, Gregory J.
Hinkle, Joseph E.
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Rastelli, Luca;
Rieger, Daniel K.;
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                                                                                                                                                                                                                                             100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Tatiana A.;
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Pred. No. 0.00078;
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APPLICANT:

APPLICANT: APPLICANT:

Krasomil-Osterfeld, Karina

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US-10-408-765A-3010
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Best Local Similarity 54.5
                                                                                                                                                                                                               Sequence 1720, Appli
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3010:
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SEQ ID NO 4590
LENGTH: 475
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                                   APPLICANT: Wu, Wei
APPLICANT: Maolong, Lu
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 30-77(52900)E
CURRENT APPLICATION NUMBER: US/10/613,520
CURRENT FILING DATE: 2003-07-02
PRIOR APPLICATION NUMBER: US 60/365,301
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CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                          APPLICANT: Monsanto Technology, LLC APPLICANT: Laurie, Cathy C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE:
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ITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
ITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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ITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
ILE REFERENCE: 38-21(51847)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity les 7; Conserv
         FILING DATE: 2002-03-15
APPLICATION NUMBER: US 10/389,566
FILING DATE: 2003-03-14
                                                                                                                                                                                                                                                                                                                       175 HQSHWQAKSLL 185
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                                                                                                                                                                                                                                                                                                                                                             HRIHWESASLL 13
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Taylor, Steven W.
Glenn, Gary M.
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                                                                                                                                                                                                                                                                                                                                                                                                                  57.1%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
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Query Match
Best Local Similarity
Matches 6; Conserva
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; OTHER INFORMATION: GenBank No.
US-09-319-724B-19
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                                                                                                                                                                                                                                     RESULT 10
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                                                                                                                                               Sequence 7603, Application U
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
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APPLICANT:
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APPLICANT: MOROOKA, Shigeaki
TITLE OF INVENTION: MANMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS
FILE REFERENCE: 53356-5001-US
CURRENT APPLICATION NUMBER: US/09/319,724B
CURRENT FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: EP 96402719.7
PRIOR PILING DATE: 1996-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
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                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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               CANT: Spiridonov, Sergei
OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
REFERENCE: 38-21(51847)B
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                                                             Goldman, Barry S.
Hinkle, Gregory J.
Huesing, Joseph E.
Malvar, Thomas M.
Krasomil-Osterfeld,
Slater, Steven C.
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NUMBER: US/09/897,516A
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75.0%;
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Pred. No.
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Pred. No.
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US-09-319-724B-5
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GENERAL INFORMATION:
APPLICANT: Brunkow, Mary E.
APPLICANT: Galas, David J.
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PRIOR APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8415
SEQ ID NO 7663
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APPLICANT: SUGASAWA, Toshinari
APPLICANT: WOROOKA, Shigeaki
TITLE OF INVENTION: MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS
FILE REFERENCE: 53356-5001-US
CURRENT APPLICATION NUMBER: US/09/319,724B
CURRENT FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: EP 96402719.7
PRIOR PILING DATE: 1996-12-12
PRIOR APPLICATION NUMBER: PCT/EP97/07339
PRIOR PILING DATE: 1997-12-12
APPLICANT: Van Ness, Jeffrey
APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
TITLE OF INVENTION: INCREASING BONE MINERALIZATION
FILE REFERENCE: 240083.508C2
CURRENT APPLICATION NUMBER: US/10/463,190
CURRENT FILING DATE: 2003-06-16
NUMBER OF SEQ ID NOS: 143
SOFTWARE: FastSEQ for Windows Version 3.0
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                       APPLICANT:
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TYPE: PRT
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nes 8; Conserv
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Similarity 85.7%;
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                                                                                                                                                                     Kovacevich, Brian
Mulligan, John T.
Paeper, Bryan W.
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Pred. No. 79
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Query Match
Best Local Similarity 50.00.
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-319-724B-1
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US-10-616-263-26
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US-09-319-724B-1
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LENGTH: 267
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GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
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APPLICANT: LENZEN,
APPLICANT: STROSBEI
APPLICANT: SUGASAW
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Best Local
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APPLICANT: SUGASAWA, Toshinari
APPLICANT: SUGASAWA, Toshinari
APPLICANT: MOROOKA, Shigeaki
TITLE OF INVENTION: MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS
FILE REFERENCE: 53356-5001-US
CURRENT APPLICATION NUMBER: US/09/319,724B
CURRENT FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: EP 96402719.7
PRIOR APPLICATION NUMBER: EP 96402719.7
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 21
             TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM FILE REFERENCE: 00766,000103.5 CURRENT APPLICATION NUMBER: US/10/616,263 CURRENT FILING DATE: 2003-07-08 NUMBER OF SEQ ID NOS: 240
                                                                                                APPLICANT:
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PatentIn
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                                                                                              Fechtel, Kim
Genetics Institute,
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Spaulding, Vikki
Wong, Gordon G.
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Treacy, Maurice
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Collins-Racie, Lisa A.
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Pred. No.
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Pred. No. 40;
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RESULT 16
US-09-319-724B-15
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US-10-616-263-26
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LENGTH: 545
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PRIOR FILING DATE: 1996-12-12
PRIOR APPLICATION NUMBER: PCT/EP97/07339
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
                                                                       SOFTWARE: PatentIn version 3.1 SEQ ID NO 15
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Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                    APPLICANT: STROSBERG, Arthur Donny
APPLICANT: SUGASAWA, Toshinari
APPLICANT: SUGASAWA, Toshinari
APPLICANT: MOROOKA, Shigeaki
TITLE OF INVENTION: MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS
FILE REFERENCE: 53356-5001-US
CURRENT APPLICATION NUMBER: US/09/319,724B
CURRENT FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: EP 96402719.7
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
RUMBER OF SEQ ID NOS: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: STROSBERG, Arthur Donny
APPLICANT: SUGASAWA, Toshinari
APPLICANT: MOROCKA, Shigeaki
TITLE OF INVENTION: MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS
FILE REFERENCE: 53356-5001-US
CURRENT APPLICATION NUMBER: US/09/319,724B
CURRENT FILING DATE: 2003-07-24
                                                                                                                                                                                                                                                                                                                                              APPLICANT: VETIGEN
APPLICANT: LENZEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
              TYPE: PRT
ORGANISM: Homo sapiens
EATURE:
                                                     ENGTH: 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 52.9%;
Local Similarity 85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 HRIHWES 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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Pred. No. 86;
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Pred. No.
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RESULT 17
US-10-603-108-2858
; Sequence 2858, Application US/10603108
; GENERAL INFORMATION:
; APPLICANT: GARY L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARE; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
Query Match
Best Local Similarity
Matches 6; Conserva
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                                                                                  ; TYPE: PRT; ORGANISM: Xenorhabdus sp. US-09-897-516A-5850
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US-09-897-516A-5850
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US-10-603-108-2858
                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/897,516A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8415
SEQ ID NO 5850
LENGTH: 677
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5850, Application US/09897516A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.9%;
Best Local Similarity 50.0%;
Matches 6; Conservative
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Matches 6; Conserv
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APPLICANT:
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CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US 09/540,263
PRIOR FILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: US 60/125,416
PRIOR APPLICATION NUMBER: US 60/125,416
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 3840
                                                                                                                                                                                                                                                             APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome
FILE REFERENCE: 38-21(51847)B
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Corbin, David R. APPLICANT: Goldman, Barry APPLICANT: Hinkle, Gregory
                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                            Goldman, Barry S.
Hinkle, Gregory J.
Huesing, Joseph E.
Malvar, Thomas M.
Krasomil-Osterfeld, Karina C.
                  Conservative
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                                  52.9%;
75.0%;
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85.7%;
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    Mismatches

                                    Score 37; DB 5;
Pred. No. 1e+02;
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                                                 Length 677;
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                                                                                                                                        US-10-624-932-26
                                                                                                                                                                                                                                                                                         Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 61 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 26
                                                                     Matches
                                                                                                     Query Match
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PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 60/221,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding FILE REPERENCE: 21402-074 US CURRENT APPLICATION NUMBER: US/10/624,932 CURRENT FILING DATE: 2003-07-21
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                                                                                                                                                     NAME/KEY: VARIANT
LOCATION: (1185)
OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
OTHER INFORMATION: specification
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                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                         ENGTH: 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OR APPLICATION NUMBER: 60/221,409
OR FILLING DATE: 2000-07-28
OR APPLICATION NUMBER: 60/222,840
OR FILLING DATE: 2000-08-04
OR APPLICATION NUMBER: 60/223,752
OR FILLING DATE: 2000-08-08
                                                                   Local Similarity les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/225,470 FILING DATE: 2000-08-15
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/225,392 FILING DATE: 2000-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/225,146 FILING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/223,769 FILING DATE: 2000-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-08-08
APPLICATION NUMBER: 60/223,770
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 428
                                 3 HRIHWESASLL 13
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Rastelli, Luca
Spaderna, Steven
Shimkete, Richard
Zerhusen, Bryan
HRFHWSRCSKL 438
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Gerlach, Valerie
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MacDougall, Johr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smithson,
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                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Vladimir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Raymond
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                                                                                   52.9%;
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                                                                   <u>,</u>
                                                                                   Score 37;
Pred. No.
                                                                   Mismatches
                                                            1.8e+02;
                                                                                                                                                                                                                                                                                                                                          See File Wrapper or PALM
                                                                                                 Length 1210;
                                                                   Indels
                                                                 Gaps
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APPLICANT:

APPLICANT:

Harlocker, Susan L.

Mitcham, Jennifer L.

APPLICANT:

Jiang, Yuqiu Henderson, Robert A. Kalos, Michael D.

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RESULT 21
PCT-US02-14753A-707
FCT-US02-14753A-707
FSQUENCE 707, Application PC/TUS0214753A
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
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US-10-467-042-4
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GENERAL INF
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SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 6; Conserv
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APPLICANT: LEE, Sally; SWARNAKAR, Anita;
APPLICANT: TRAN, Uyen K.; XU, Yuming
APPLICANT: TRAN, Uyen K.; XU, Yuming
TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES
FILE REFERENCE: PI-0361 USN
CURRENT APPLICATION NUMBER: US/10/467,042
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: PCT/US02/02813
PRIOR APPLICATION NUMBER: DCT/US02/02813
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: US 60/266,762
PRIOR APPLICATION NUMBER: US 60/266,762
PRIOR APPLICATION NUMBER: US 60/266,762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/275,586
PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: US 60/278,505
PRIOR FILING DATE: 2001-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/269,581
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/271,198
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2001-03-01
PRIOR FILING DATE: 2001-03-01
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 1719204CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1221
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                434 HRFHWSRCSKL 444
                                                                                                                                                                                                                                                                             3 HRIHWESASLL 13
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DUGGAN, Brendan M.; HAFALIA, April J.A.;
ARVIZU, Chandra S.; THANGAVELU, Kavitha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRIFFIN, Jennifer A.; GIETZEN, Kim
LU, Dyung Aina M.; ISON, Craig H.;
RAMKUMAR, Jayalaxmi; TANG, Y. Tom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GANDHI, Ameena R.; BAUGHN, GRIFFIN, Jennifer A.; GIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YAO, Monique G.; ELLIOTT, Vicki S.; DING, Li; YUE, Henry;
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Program
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                                                                                                                                                                                                                                                                                                                                                    52.9%;
                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 6;
Pred. No. 1.8e+02;
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PPLICANT:

'edvick,

Thomas

Craig H.

Fanger, Gary R. Retter, Marc W. Stolk, John A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.4725PC CURRENT APPLICATION NUMBER: PCT/US02/14753A CURRENT FILING DATE: 2002-05-09 NUMBER OF SEQ ID NOS: 103 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 707 LENGTH: 150 TYPE: PRT
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                            PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR APPLICATION NUMBER: 19/837,944
PRIOR FILING DATE: 2001-04-18
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les 5; Conserv
APPLICATION NUMBER: 60/338,692 FILING DATE: 2001-12-11
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                                                                                                                                                                                                                                                                         Pilgrim, Marsha L
Dubell III, Arnold T
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Riechmann, Jose Luis
Jiang, Cai-Zhong
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Hepler, William T.
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Broun, Pierre E
                                                                                                                                                                                                                                                                                                                                                                                                                   Haake, Volker
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Vinals y de Bassols,
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                                                                                                                                                                                                                                                                                                                                            T. Lynne
                                                                                                                                                                                                                                                                                                                                                                                                   , Robert A
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PRIOR APPLICATION NUMBER: 10/225,066
PRIOR FILING DATE: 2002-08-09
PRIOR PPLICATION NUMBER: 10/225,067
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: Patentin version 3.2
SEQ ID NO 2864
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US-10-603-114-4493
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                                                                                                                                                                                                                                                                                   US-10-293-244-1738
                                                                                                                                                                                                                                                                                                        RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-603-114-4493
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SEQ ID NO 4493
LENGTH: 346
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Best Local Similarity
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GENERAL INFORMATION:
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              CURRENT APPLICATION NUMBER: US/10/293,244
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: Not Yet Assigned
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/603,114
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/543,681
PRIOR FILING DATE: 2000-04-05
                                                                                                                                                                   APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y. Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILITILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2002-06-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
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09/663,561
                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
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Pred. No.
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Pred. No.
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CURRENT APPLICATION UMBER: US/10/612,783
CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 7098
SEQ ID NO 5264
LENGTH: 356
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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US-10-293-244-3486
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PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53373)A
GUIDDREW ADDITION WITH STANKING TO THE TOTAL WITHOUT TO THE TOTA
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SOFTWARE: Custom
SEQ ID NO 1738
                                                                                                                                                                                                                                                                                                                                                           Sequence 3486, Application US/10293244 GENERAL INFORMATION:
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Best Local :
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APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y. Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-029
CURRENT APPLICATION NUMBER: US/10/293,244
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: Not Yet Assigned
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR FILING DATE: 2000-11-30
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TYPE: PRT
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5; Conserve
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Pred. No.
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Pred. No.
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                                                                                                                                                                          ; ORGANISM: Homo sapiens US-10-293-244-1518
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/293,244
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: Not Yet Assigned PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR FILING DATE: 2000-01-020
PRIOR APPLICATION NUMBER: 09/663,561
PRIOR FILING DATE: 2000-09/654,936
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/650,325
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US-10-293-244-1518
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SOFTWARE: CUBL.
SEQ ID NO 3486
'SNGTH: 272
                                                                        Query Match 50.7%;
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                            SEQ ID NO 1518
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y. Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 21272-029
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PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
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PRIOR FILING DATE: 2000-02-03
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                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/496,914
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
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TYPE: PRI
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2 THR-----IHWESASLL :|| | | | | | |
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Pred. No. 72;
1; Mismatches
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                                                                                                  Score 35.5;
Pred. No. 9:
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SHRPVGMDIHWEKVSKL 271

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RESULT 30
US-10-603-113-15056
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US-60-485-450-927
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US-10-408-765A-2327
Sequence 15056, Application US/10603113
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 927
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2327
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Best Local Similarity 47.1%;
Matches 8; Conservative
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APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GREATIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN I
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF I
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001470
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2003-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/408,765A CURRENT FILING DATE: 2003-04-04
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TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
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APPLICANT: Fahy, Eoin D.
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TYPE: PRT
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                   Score 35; DE
Pred. No. 30;
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Pred. No. 9
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METHODS OF DETECTION AND USES
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; ORGANISM: Proteus mirabilis US-10-603-114-6463
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US-10-603-114-4555
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GENERAL INFORMATION:
APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

FULE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/10/603,114

CURRENT FILING DATE: 2003-06-24

PRIOR APPLICATION NUMBER: US/09/543,681

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09
                         APPLICATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILITIE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/10/603,114
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/543,681
PRIOR FILING DATE: 1909-04-05
PRIOR FILING DATE: 1999-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6463
LENGTH: 337
TYPE: PRT
                                                                                                                                                                                                                                                                                                                         Sequence 6463, Application US/10603114 GENERAL INFORMATION:
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SEQ ID NO 4555
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Best Local
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PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
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CURRENT FILING DATE: 2003-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 107196.132
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TYPE: PRT
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5; Conserv
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Pred. No.
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Pred. No.
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Query Match

50.0%;

Score 35;

DB 6;

Length 337;

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RESULT 35
PCT-US02-29560A-205
; Sequence 205, Application PC/TUS0229560A
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US-60-487-610-1550
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TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1310
LENGTH: 1086
TYPE: PRT
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CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1550
LENGTH: 566
                                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local
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APPLICANT:
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APPLICANT: HUANG, Hongjin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
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ORGANISM: Homo sapiens
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                                                                                  LLHLIHWE 91
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Taylor, Steven W.
Glenn, Gary M.
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Pred. No. 1.8e
0; Mismatches
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                                                                                                                                                              Score 35; DB 6;
Pred. No. 3.5e+02;
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US-10-612-783-6253
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                                                                                                                Sequence 6253, Application US/10612783 GENERAL INFORMATION:
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APPLICANT: Aziz, Natas
APPLICANT: Gish, Kurt
APPLICANT: Hevezi, Pet
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    TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(53373)A
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ORGANISM: Homo sapiens
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Gish, Kurt C.
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Mack, David H.
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APPLICANT: CARGILL, Michele
APPLICANT: HUANG, Hongiln
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FAST-SEQ FOR WINDOWS Version 4.0
SEQ ID NO 1551
LENGTH: 1211
TYPE: PRT
ORGANISM: Homo sapiens
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TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Diagnosis of Cancer of Cancer
FILE REFERENCE: 018501-002710PC
CURRENT APPLICATION NUMBER: PCT/US02/29560A
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: US 60/323,469
PRIOR FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 412
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 205
LENGTH: 1211
APPLICANT: Kovali, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 7;
Pred. No. 3.9e+02;
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Pred. No. 3.9e+02;
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US-10-637-011-21
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CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 3264
SOFTWARE: PatentIn version 3.2
SEQ ID NO 778
LENGTH: 213
TYPE: PRT
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CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 7098
SEQ ID NO 6253
LENGTH: 210
TYPE: PRT
                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/10637011 GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity 62.5%;
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APPLICANT: Chiron Corporation
TITLE OF INVENTION: Neisseria Meningitidis Antigens and Compositions
FILE REFERENCE: CHIR-0334
                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                              APPLICANT: JESTIN
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LOCATION: (1)..(210)
OTHER_INFORMATION: unsure at all Xaa locations
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NAME/KEY: misc_feature
LOCATION: (23)..(23)
OTHER INFORMATION: Xaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 HRFHWACA 182
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                                                                                                                                             ALBINA, Emanuel
Le CANN, Pierre
BLANCHARD, Phillipe
HUTET, Evelyne
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ARNAULD, Claire
TRUONG, Catherine
MAHE, Dominique
CARIOLET, Roland
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Pred. No. 1e+02;
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Pred. No. 98;
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Query Match
Best Local Similarity
Watches 4; Conserva
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                                                                                                                                                    ; TYPE: PRT ; ORGANISM: Oryza sativa US-10-613-520-797
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US-10-613-520-797
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                                                                        Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                               SOFTWARE: Pa
SEQ ID NO 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
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SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 797,
                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 2578
                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FILING DATE: 2002-06-26
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/613,520
CURRENT FILING DATE: 2003-07-02
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 10/389,566
PRIOR FILING DATE: 2003-03-14
PRIOR FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: US 60/391,786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Maolong, Lu
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77(52900)E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR FILING DATE: 1997-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/637,011
CURRENT FILING DATE: 2003-08
PRIOR APPLICATION NUMBER: US/09/514,245B
PRIOR FILING DATE: 2000-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS TITLE OF INVENTION: DISEASE (PWD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 065691/0176
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TYPE: PRT
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RLHWERRGLV
                                   RIHWESASLL 13
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Pred. No. 2.7e+02;
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Search completed: August 28, 2003, 14:21:50 Job time: 24 secs

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AAW34624 AAW34629	ABG25976 AAW34623	ABB82769 ABU08618	ABU08617	ABP58087	ID
Human C3 protein m Human C3 protein m	Novel human diagno Human C3 protein m	Congestive heart f Disease specific b	Disease specific b	Complement C3f fra	Description

Biopolymer marker useful for evidencing, categorizing or regulating least one disease state, e.g. congestive heart failure, myocardial

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16		14	13	12	11	10
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ABP29330	ABB69833	AAG15895	ABP10890	ABB54019	ABB58617	ABG72971	ABU08967	AAW34631	AAW34626	AAW34618	AAW34617	AAW34616	AAW34615	AAW34614	AAW34613	AAW34612	AAW34611	AAW34610	AAW34609	AAW34608	AAW34607	AAW34606	AAW40990	AAW40989	AAW40988	AAW34630	AAW34628	AAW34627	AAW34621	AAW34620 .	AAW34619	AAR94030	AAR94029	AAR94028	AAW34625
Streptococcus poly	Drosophila melanog	Arabidopsis thalia	Human ORFX protein	Lactococcus lactis	phila melano	Human complement C		Human C3 protein m	C	C	C	ជ	C3 protein	C	C3 prote	C	C C	C3 protein	C	Human C3 protein m	r C3 p	type	Human C3 protein m	C	C	C	C3 protein	C3 protein	C	C3 protein	C3 protei	_	modified	ဌ	Human C3 protein m

ALIGNMENTS

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RESULT 1
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                                                                                                                              WPI; 2003-111907/10.
                                                                                                                                                                                                                  Jackowski G,
                                                                                                                                                                                                                                                                                                                                                                                                     30-APR-2001; 2001US-0845730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-APR-2002; 2002WO-CA00617.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complement C3f fragment, specific disease marker.
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Claim 1; infarction or

Page 30; 30pp; English

intracerebral hemorrhage

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Best Local (
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                                                                                                                                                                                                                                                                                                                                                 diabetes; kluney ... stroke; C3f; complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in indicating at least one particular disease state. The marker is a C3f fragment from the complement system having a mol.wt. of about 1690 Da. The marker is indicative of an individual suffering from myocardial infarction, intracerebral haemorrhage or congestive heart failure. The invention involves the use of a combination of
                                                                                                                                                                                                                                                                              31-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                          Biopolymer; disease state; congestive heart failure; asymptomatic; diabetes; kidney failure; heart failure; Syndrome X; heart attack;
                                                                                                                                                                                                                                                                                                                                                                                                                  Congestive heart failure C3f fragment marker bioploymer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG75803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG75803 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
             Claim 1;
                                       disease state
                                                                                                          Jackowski G,
                                                                                                                                                                                                                       30-APR-2001; 2001US-0845739
                                                                                                                                                                                                                                                  30-APR-2001; 2001US-0845739
                                                                                                                                                                                                                                                                                                          US2002160419-A1.
                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                    (THAT/)
(MARS/)
(YANT/)
                                                                                                                                                                                              (JACK/)
                                     novel biopolymer marker useful in indicating at least isease state particularly congestive heart failure -
                                                                               2003-246643/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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                                                                                                                                                  THATCHER B.
MARSHALL J.
YANTHA J.
                                                                                                                                                                                             JACKOWSKI G.
                                                                                                                                       VREES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
           Page 7; 10pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence is that of a biopolymer marker that is useful
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                                                                                                           Thatcher
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                                                                                                          Marshall J,
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Pred. No. 3.4e-05;
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                                                                                                           Yantha
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Best Local S
Matches 13
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                                                       least one particular disease state. (I) is useful for indicating a disease state, in particular type II diabetes. The marker sequences are useful as antigens in immunoassays for the detection of those individual suffering from the disease known to be evidenced by the marker sequence. (I) provides an efficient diagnostic tool for rapidly and accurately diagnosing disease states such as type II diabetes. This is the amino acid sequence of a biopolymer marker.
                                                                                                                                                                                                                                                                                                                                                                                                                          Biopolymer marker useful in indicating disease state, in particular type II diabetes and as antigens in immunoassays for detecting individuals suffering from disease known to be evidenced by marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention discloses a biopolymer marker which is useful in indicate at least one particular disease state, particularly congestive heart failure. The polymer marker is also useful for characterising disease states. The polymer marker allows physicians to identify asymptomatic states. The polymer marker allows physicians to identify asymptomatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disease specific biopolymer marker #1.
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                                                                                                                                                                                                                                                                        The invention describes a biopolymer marker (I) useful in indicating
                                                                                                                                                                                                                                                                                                                                   Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                    type II diabetes and as antigens in individuals suffering from disease k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-328370/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jackowski G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JACK/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biopolymer marker; type II diabetes; immunoassay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAY-2003
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MARSHALL J.
YANTHA J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JACKOWSKI G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                   English.
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Pred. No.
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3.7e-05;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a biopolymer marker of the invention and is a disease specific marker. The marker is characterised as a C3f fragment from the complement system having a molecular weight of about 2056 daltons. The biopolymer marker identified is useful for evidencing, categorizing or regulating at least one disease state, preferably congestive heart failure.
Biopolymer marker; type II diabetes; immunoassay.
                                               Disease specific biopolymer marker
                                                                                                                                                  ABU08618;
                                                                                                                                                                                               ABU08618 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of biopolymer marker for evidencing, categorizing or regulating least one disease state, e.g. congestive heart failure \,
                                                                                                  23-MAY-2003
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ilarity 100.0%;
Conservative (
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Pred. No. 4.2e-05;
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RESULT 6
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a biopolymer marker (I) useful in indicating at least one particular disease state. (I) is useful for indicating a disease state, in particular type II diabetes. The marker sequences are useful as antigens in immunoassays for the detection of those individual suffering from the disease known to be evidenced by the marker sequence. (I) provides an efficient diagnostic tool for rapidly and accurately diagnosing disease states such as type II diabetes. This is the
                                             31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forension food supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                         30-MAR-2001; 2001WO-US08631
                                                                                                                                                                               11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #25967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biopolymer marker useful in indicating disease state, in particular type II diabetes and as antigens in immunoassays for detecting individuals suffering from disease known to be evidenced by marker sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JACK/)
                                                                                                                                                                                                                                WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG25976 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2; 10pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-APR-2001; 2001US-0846346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-2002.
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13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THATCHER MARSHALL YANTHA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VREES T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JACKOWSKI G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of a biopolymer marker.
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Pred. No.
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RESULT 7
AAW34623
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polymcleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polymucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                      Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drmanac RT,
                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human C3 protein mutant FT-1.
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                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW34623 standard; Protein; 1592 AA
                       WO9732981-A1
                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                   1592
                                                                                                                                                                                                Location/Qualifiers
                                                                                                    1593
                                                                       /note= "A1593Stop mutation'
                                                                                                                      'note= "E1592N mutation"
                                                                                                                                                                        note= "R1591T mutation"
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Pred. No. 0.0064;
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                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified complement pathway protein that forms C3 convertage resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of th invention, and is a modified native complement pathway protein (A) th forms a down-regulation resistant C3 convertase. (A), their variants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 17; Page -; 123pp; English.
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                                                                 complement-mediated disease; autoimmune disease; leukaemia cell; complement-mediated response; MHC-mismatched lymphocyte; mutein.
                                                                                 down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour;
                                                                                                                     Human; C3 protein; convertage; complement pathway protein;
                                                                                                                                                       Human C3
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                                                                                                                                                       protein mutant FT-2.
                                                                                                                                                                                                                                                          standard; Protein; 1635 AA
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96GB-0011896.
96GB-0014293.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 70; DB 18;
Pred. No. 0.0066;
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Location/Qualifiers

Misc-difference 1636

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Best Local S
Matches 13
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07-MAR-1996;
07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                   (particularly a xenograft) but also to prevent complement mediated diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous virus, infected conversion and deposition at a specific site (e.g. a virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating any cancer cells left after surgical removal of a tumour). Also contemplated is ex vivo treatment, especially by passing blood through a matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or MHC-mismatched lymphocytes in extracted bone marrow. Since (A) is not inhibited by factor I, it can bind repeatedly to factor B (which is then inactivated), causing inactivation of the alternative pathway by consumption of factor B.
Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (see AAW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A) their variants, fragments and conjugates are used to deplate levels of complement pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material contents to prevent rejection of section material
                                                                      Human C3 protein mutant FR-2.
                                                                                                          09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                         inactivated), caucinactivated) factor
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                                                                                                                                                                                                                                                                 1307
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                                                                                                                                                                                                                                                                                                  μ.
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                                                                                                                                                                                                                                                              ITHRIHWESASLL 1319
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                                                                                                                                                                                                                                                                                                                                  Conservative
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96GB-0011896.
96GB-0014293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96GB-0024028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-GB00603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "wild type E mutated to stop codon"
                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                Score 70; DB 18;
Pred. No. 0.0068;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                  <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                 Length 1635;
                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                0
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RESULT 10
AAW34625
ID AAW34
XX
AC AAW34
XX
DT 09-AE

AAW34625;

AAW34625

standard;

Protein; 1661 AA

0

09-APR-1998

(first entry)

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                             S
                                                                                                                                 Matches
                                                                                             Query Match
                                                                                                                                                                                                                                                                          forms a down-regulation resistant C3 convertase. (A), their variants, fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement mediated diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a virus, infected cell or tumour, to increase sensitivity to complement—mediated responses; a particular application is eliminating any cancer cells left after surgical removal of a tumour). Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a mutated human C3 protein of the invention, and is a modified native complement pathway protein (A) that invention, and is a modified native complement pathway protein (A) that
                                                                                                                                                                                                                             contemplated is ex vivo treatment, especially by passing blood through matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft
                                                                                                                              Sequence
                                                                                                                                                                               MHC-mismatched lymphocytes in extracted bone marrow. Since (A) is no inhibited by factor I, it can bind repeatedly to factor B (which is inactivated), causing inactivation of the alternative pathway by
                                                                                                                                                               inactivated), causing consumption of factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 17; Page -; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-457534/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Farries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9732981-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement-mediated response; MHC-mismatched lymphocyte; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMUT-) IMUTRAN LTD.
                                                                               Local
 1307
                                                            ch 100.0%;
1 Similarity 100.0%;
13; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĭĊ,
                               ITHRIHWESASLL 13
ITHRIHWESASLL 1319
                                                                                                                                1657 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96GB-0024028.
96GB-0004865.
96GB-0011896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96GB-0014293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1638..1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "wild type residues QDEENQKQ mutated
                                                                                                                                                                  ₩.
                                                                0
                                                                             Score 70;
Pred. No.
                                                                red. No. 0.0069;
Mismatches 0
                                                                                               DB 18;
                                                                0
                                                                                             Length 1657;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                               (A) is not
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                                                                Gaps
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C

protein mutant FT-3.

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RESULT 11
AAR94028
ID AAR94
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                                                                                                                                                                                                                                        This sequence represents a mutated human C3 protein of the invention CC (see AAW34606 for wild type protein). This protein is a protein of the cinvention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, CC fragments and conjugates are used to deplete levels of complement c2 pathway proteins (by superactivation until one or more components are CC exhausted), specifically to prevent rejection of foreign material CC (particularly a xenograft) but also to prevent complement-mediated c1 exhausted), specifically to prevent complement-mediated c2 complement protein conversion and deposition at a specific site (e.g. a c2 complement protein conversion and deposition at a specific site (e.g. a c2 complement-mediated responses; a particular application; Also C2 complement-mediated responses; a particular application; Also C3 contemplated is ex vivo treatment, especially by passing blood through a c2 contemplated is ex vivo treatment, especially by passing blood through a c3 contemplated is ex vivo treatment, especially by passing blood through a c2 contemplated by phocytes in extracted bone marrow. Since (A) is not c1 inhibited by factor I, it can bind repeatedly to factor B (which is then c1 can sumption of factor B. c2 consumption of factor B.
                                                                                                                                                 Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
   AAR94028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-457534/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Farries TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 17; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rejection, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9732981-A1
                                                                                   1307
                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMUTRAN LTD.
                                                                                                                                                                Similarity
 standard;
                                                                                                                ITHRIHWESASLL 13
                                                                                 ITHRIHWESASLL 1319
                                                                                                                                                                                                                1661 AA;
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96GB-0024028.
96GB-0004865.
96GB-0011896.
96GB-0014293.
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1607..1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -; 123pp;
Protein; 1663 AA
                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "wild type residues LSSDFWGE mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                 0
                                                                                                                                                                Score 70;
Pred. No.
                                                                                                                                                 Mismatches
                                                                                                                                                                DB 18;
0.0069;
                                                                                                                                                 0
                                                                                                                                                                              Length 1661;
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                                                                                                                                                 Gaps
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RESULT 12
AAR94029
ID AAR94
XX
AC AAR94
XX
DT 21-MA
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                                                                                                                                                                                            Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                Human C3 protein (AAR94028) was produced by expression of a cDNA sequence (AAT17738) isolated from a human liver cDNA library. C3 is a complement pathway protein that is complement colleavage by Factor I and is also susceptible to the inhibitory action of Factor H. Mutants of C3 (AAR94029 and AAR94030) have been produced by site-directed mutagenesis. These mutants can be
                       AAR94029;
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                               used to super-active the complement system, or to induce localised super-activation at a specific target to increase the target's sensitivity to complement-mediated destruction
                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                Mutant complement pathway protein forming stable C3 convertase for generalised complement depletion or localised complement
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-171613/17.
N-PSDB; AAT17738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-1995;
08-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-1996
                                            AAR94029
                                                                                                                                                                                                                                                                                                                                                                                                                                    Farries TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human C3 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR94028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMUT-) IMUTRAN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                               Local Similarity nes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; convertase; Factor I; Factor H; complement
                                                                                                    1307
                                            standard; Protein; 1663 AA
                                                                                                                  ITHRIHWESASLL 13
                                                                                                                                                                                            1663 AA;
                                                                                                                                               100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                    Harrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95GB-0009102.
94GB-0018147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-GB02121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 672..1663
/note= "C3 alpha chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         668..671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label≃ Sig_peptide
?3..667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "C3 beta chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "amino acids 668-671 are removed when the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      precursor is cleaved beta chains"
                                                                                                                                                0;
                                                                                                                                             Score 70; DB 17;
Pred. No. 0.0069;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    into
                                                                                                                                                  0
                                                                                                                                                                     Length 1663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the alpha and
                                                                                                                                                0,
                                                                                                                                                Gaps
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21-MAY-1996

(first entry)

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RESULT 13
AAR94030
ID AAR94
XX
AC AAR94
XX
DT 21-MA
XX
DE Human
                                                                                         밁
                                                                                                       S
                                                                                                                                                            Query Match
Best Local S
Matches 13
                                                                                                                                                                                                 A modified human C3 protein (AAR94029) differs from the wild-type (AAR94028) by substitution of Arg-1303 by glutamic acid, glycine or glutamine. It is obtained by site-directed mutagenesis of C3-encoding cDNA (AAT17738). The modification results in improved resistance to cleavage by Factor I in comparison to wild-type C3. This allows the modified C3 to be used therapeutically to
                                                                                                                                                                                                                                                                             Mutant complement pathway protein forming stable C3 convertase for generalised complement depletion or localised complement activation
Human modified C3 (D752G, E753S, D754G).
                                                                                                                                                           Sequence
                                                                                                                                                                                  super-active the complement system or the increase a target's (e.g. tumour, pathogen or virus-infected cell) sensitivity to
                                                                                                                                                                                                                                                                                                                                                               04-MAY-1995;
08-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                 21-MAY-1996
                                  AAR94030;
                                               AAR94030 standard; Protein; 1663
                                                                                                                                                                            complement-mediated
                                                                                                                                                                                                                                                            Claim 8; Fig 1; 81pp; English.
                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                               Farries
                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                        WO9607738-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C3 protein;
tumour; info
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human modified
                                                                                                                                                                                                                                                                                                                                               (IMUT-)
                                                                                          1307
                                                                                                                                                                                                                                                                                                              1996-171613/17
                                                                                                          μ
                                                                                                                           l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                              TC,
                                                                                                                                                                                                                                                                                                                                               IMUTRAN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection; therapy
                                                                                         ITHRIHWESASLL 1319
                                                                                                        ITHRIHWESASLL 13
                                                                                                                                                            1663 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               convertase; Factor I; Factor H; complement;
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                              Harrison
                (first entry)
                                                                                                                                                                                                                                                                                                                                                              95GB-0009102.
94GB-0018147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C3 (R1303X).
                                                                                                                                                                                                                                                                                                                                                                                        95WO-GB02121
                                                                                                                                                                                                                                                                                                                                                                                                                                                672..1663
/note= "C3 alpha chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  668..671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Glu, Gly, Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "C3 beta chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Sig_peptide
23..667
                                                                                                                                 100.0%;
                                                                                                                                                                            destruction.
                                                                                                                                                                                                                                                                                                                              RA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "amino acids 668-671 are removed when the precursor is cleaved into the alpha and beta chains"
                                                                                                                           0
                                                                                                                                 Score 70; DB 17;
Pred. No. 0.0069;
                                                                                                                          Mismatches
                                                 ₹
                                                                                                                                         Length 1663;
                                                                                                                           Indels
                                                                                                                           0
                                                                                                                         Gaps
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RESULT 14
AAW34
ID AAW34
XX AAW34
AC AAW34
XX O9-AE
XX U9-AE
XX Human
XX Human
KW down-
KW compl
                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AAR94028) by substitution of Asp-Glu-Asp at positions 752-754 igly-Ser-Gly. It is obtained by site-directed mutagenesis of C3-encoding cDNA (AAR17738). The modification reduces the interaction of C3b/C3i with Factor H in comparison to wild-type C3. This allows the modified C3 to be used therapeutically to super-active the complement system or the increase a target's (e.g. tumour, pathogen or virus-infected cell) sensitivity to complement-mediated destruction.
Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A modified human C3 protein (AAR94030) differs from the wild-type
                                                                           Human C3
                                                                                                                09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Fig 1; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant complement pathway protein forming stable C3 convertase for generalised complement depletion or localised complement
                                                                                                                                                                                   AAW34619 standard; Protein; 1663 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-171613/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Farries TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-1995;
08-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAR-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C3 protein; infection; t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMUT-) IMUTRAN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                  1307
                                                                                                                                                                                                                                                                                                                       ب
                                                                                                                                                                                                                                                                                                                                                          l Similarity
                                                                           protein
                                                                                                                                                                                                                                                                                                                     ITHRIHWESASLL 13
                                                                                                                                                                                                                                                                                ITHRIHWESASLL 1319
                                                                                                                                                                                                                                                                                                                                                                                                                                  1663 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     convertase; Factor I; Factor H; complement; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harrison
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        precursor is the beta chains 672..1663 /note= "C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95GB-0009102.
94GB-0018147.
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                                                                           mutant DV-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "C3 beta chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "C3 alpha chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "amino acids 668-671 are removed when the
                                                                                                                                                                                                                                                                                                                                                          <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                         Score 70; DB 17;
Pred. No. 0.0069;
                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is cleaved into the alpha and
                                                                                                                                                                                                                                                                                                                                                                                             DB 17;
                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                             Length 1663;
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                                                                                                                                                                                                                                                                                                                                                        Gaps
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complement-mediated

response; MHC-mismatched lymphocyte; mutein

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CC This sequence represents a mutated human C3 protein of the invention CC (see AAW34606 for wild type protein). This protein is a protein of the CC invention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, CC fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are CC exhausted), specifically to prevent rejection of foreign material CC (particularly a xenograft) but also to prevent complement-mediated CC diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous CC complement protein conversion and deposition at a specific site (e.g. a CC virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating CC contemplated is ex vivo treatment, especially by passing blood through a matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or CC (mismatched lymphocytes in extracted bone marrow. Since (A) is not inactivated), causing inactivation of the alternative pathway by CC consumption of factor B.
                                                                                                                         Query Match
Best Local
                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 14; Page -; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-457534/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Farries TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9732981-A:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rejection, etc.
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1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                           Similarity
ITHRIHWESASLL 1319
                                                ITHRIHWESASLL 13
                                                                                                                                                                                                       1663 AA;
                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harrison
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96GB-0004865.
96GB-0011896.
96GB-0014293.
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1219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "K1217E
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                                                                                                                         100.0%;
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                                                                                                                         Score 70; I
Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutation"
                                                                                                                      DB 18;
0.0069;
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                                                                                                                                                 Length 1663;
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RESULT 15 AAW34620

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This sequence represents a mutated human C3 protein of the invention CC (see AAW34606 for wild type protein). This protein is a protein of the CC invention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, CC fragments and conjugates are used to deplete levels of complement CC pathway proteins (by superactivation until one or more components are CC exhausted), specifically to prevent rejection of foreign material CC (particularly a xenograft) but also to prevent complement-mediated CC diseases resulting from (surgical) injury or antibody-antigen interaction CC in autoimmune disease, also to localise and/or amplify endogenous CC complement protein conversion and deposition at a specific site (e.g. a CC virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated lymphocytes in extracted bone marrow. Since (A) is not CC inhibited by factor I, it can bind repeatedly to factor B (which is then CC consumption of factor B.
Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathway by super-activation, especially for preventing rejection, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-457534/42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.
                                                                                                       consumption of factor B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMUT-) IMUTRAN LTD.
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100.0%;
ilarity 100.0%;
Conservative C
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96GB-0004865.
96GB-0011896.
96GB-0014293.
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Score 70; DB 18;
Pred. No. 0.0069;
Nismatches 0;
                                 Length 1663;
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RESULT 16
AAW34621
AAW34621
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virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating any cancer cells left after surgical removal of a tumour). Also contemplated is ex vivo treatment, especially by passing blood through a matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or MHC-mismatched lymphocytes in extracted bone marrow. Since (A) is not inhibited by factor I, it can bind repeatedly to factor B (which is the
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07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
                                                                                                                                                                                                                                                              forms a down-regulation resistant C3 convertage. (A), their variants, fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement mediated diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (see AAW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 14; Page -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistant to down-regulation, especially for preventing pathway by super-activation, especially for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-457534/42
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96GB-0004865.
96GB-0011896.
96GB-0014293.
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1433
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1431
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RESULT 17
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07-MAR-1996;
07-JUN-1996;
                                               This sequence represents a mutated human C3 protein of the invention (see ANM34606 for wild type protein. This protein is a protein of the invention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants, fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement-mediated diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a virus, infected cell or tumour, to increase sensitivity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inactivated), causing inactivation
consumption of factor B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; C3 protein; convertage; complement pathway protein; infection; down-regulation resistant C3 convertage; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.
     complement-mediated responses; a particular application
any cancer cells left after surgical removal of a tumou:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-457534/42
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                                                                                                                                                                                                                                                                                                                                                                                                                              Example 17; Page -; 123pp;
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96GB-0004865.
96GB-0011896.
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RESULT 18
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AC ARAW34
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PR 07-U1
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07-MAR-1996;
07-JUN-1996;
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                                                                                                                                                                            Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAR-1997;
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                                                                                                                                                                                                                                                                                    WPI; 1997-457534/42
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13; Conserv
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Pred. No. 0.0069;
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sequence represents a mutated human C3 AAW34606 for wild type protein). This I

represents a mutated human C3 protein of the invention for wild type protein). This protein is a protein of the is a modified native complement pathway protein (A) the complement (A) the complement pathway protein (A) the complement pathway pathway (A) the complement (A) the complement

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RESULT 19
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07 - MAR-1996;
07 - JUN-1996;
08 - JUL-1996;
            Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complemen pathway by super-activation, especially for preventing graft rejection, etc.
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                                                                                                                                      Farries TC,
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13; Conserv
                                                                                                                                                                        IMUTRAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITHRIHWESASLL 1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1663 AA;
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                                                                                                                                       Harrison
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                                                                                                                                                                                                         96GB-0004865.
96GB-0011896.
96GB-0014293.
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                                                                                                                                                                        LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1638..1645
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                                                                                                                                       RΑ;
                                                                                                                                                                                                                                                                                                                                                                                                        "wild type residues QDEENQKQ mutated
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                           complement
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Example 17;

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                         19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                           down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.
              Farries
                                                                                                                                                         04-MAR-1997;
                                                                                                                                                                                                                    WO9732981-A1
                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; C3 protein; convertage; complement pathway protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human C3 protein mutant R1303X, R1320X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW40988 standard; Protein; 1663 AA.
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                                            (IMUT-) IMUTRAN LTD.
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AAW34606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1663 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
              Harrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represents a mutated human C3 protein of the invention for wild type protein). This protein is a protein of the invention
                                                                         96GB-0024028.
96GB-0004865.
96GB-0011896.
96GB-0014293.
                                                                                                                                                        97WO-GB00603
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                  /label= Glu, Tyr, Cys,
                                                                                                                                                                                                                                                                               /label= Glu,
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                                                                                                                                                                                                                                                                               Tyr,
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Pred. No. 0.0069;
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                                                                                                                                                                                                                                              Trp,
                                                                                                                                                                                                                                                                            Trp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 18;
                                                                                                                                                                                                                                                   Gln, Gly
                                                                                                                                                                                                                                                                               Gln,
                                                                                                                                                                                                                                                                                 Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1663;
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                                                                                                                                                                                                                                                                                                                                                                                                                          infection;
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1307

ITHRIHWESASLL 1319

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RESULT 21
AAW40989
ID AAW40
XX
AC AAW4(
XX
DT 09-A:
XX
DT 09-A:
XX
Comp
KW Huma
KW Huma
KW Comp
KW Comp
KW Comp
XX
FH Key
FT Mis

sapiens

Misc-difference

Location/Qualifiers 1303 /label= Glu, Gln, Gly

Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.

Human C3 protein mutant R1303X 09-APR-1998 (first entry) AAW40989 standard; Protein; 1663 AA.

19-NOV-1996; 07-MAR-1996; 07-JUN-1996; 08-JUL-1996;

96GB-0004865. 96GB-0011896. 96GB-0014293. 96GB-0024028. 97WO-GB00603

04-MAR-1997;

12-SEP-1997 WO9732981-A1

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S
                                                                                                                                           This sequence represents a mutated human C3 protein of the invention CC (see AAW34606 for wild type protein). This protein is a protein of the compensation, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, CC pathway proteins (by superactivetion until one or more complement complement are certifically to prevent rejection of foreign material capacitivation until one or more components are comparated to deplete levels of complement are comparated in autoimmune disease, also to prevent complement-mediated complement protein conversion and deposition at a specific site (e.g. a crimis, infected cell or tumour, particular application is eliminating complement-mediated responses; a particular application is eliminating contemplated is ex vivo treatment, especially by passing blood through a contemplated is ex vivo treatment, especially by passing blood through a contemplated is ex vivo treatment, especially by passing blood through a contemplated is ex vivo treatment, especially by passing blood through a contemplated is ex vivo treatment, especially by passing blood through a contemplated is factor mediators) or killing of leukaemia cells or contemplated by factor T, it can bind repeatedly to factor B (which is then can bind repeatedly to factor B (which is then can bind repeatedly to factor B (which is then can bind repeatedly to factor B).
                                                Matches
                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page -; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-457534/42
                                                                        Local
                                             l Similarity
13; Conserv
1 ITHRIHWESASLL 13
                                                                                                                                           1663 AA
                                                Conservative
                                                                     100.0%;
                                                0;
                                                                     Score 70;
Pred. No. (
                                                  Mismatches
                                                                        0.0069;
                                                                                             DB 18;
                                                    0
                                                                                             Length 1663;
                                                  Indels
                                                <u>,,</u>
                                                Gaps
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RESULT 22
AAW40990
ID AAW4C
XX AAW4C
XX O9-AE
AC AAW4C
XX Humar
XX Humar
XX Humar
XX Humar
XX Homo
XX Compl
XX Compl
XX Homo
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC This sequence represents a mutated human C3 protein of the invention CC (see AAW34606 for wild type protein). This protein is a protein of the CC invention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, CC fragments and conjugates are used to deplete levels of complement CC pathway proteins by superactivation until one or more components are CC exhausted), specifically to prevent rejection of foreign material CC diseases resulting from (surgical) injury or antibody-antigen interaction CC diseases resulting from (surgical) injury or antibody-antigen interaction CC complement protein conversion and deposition at a specific site (e.g. a C virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application; aliminating CC contemplated is ex vivo treatment, especially by passing blood though a CC contemplated is ex vivo treatment, especially by passing blood though a CC matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or CC inhibited by factor I, it can bind repeatedly to factor B (which is then CC consumption of factor B.

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                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                 Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human C3 protein mutant.
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                                                                                               Misc-difference
                                                                                                                                                        Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                               /note= "D996S mutation" 997
                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                            993
   /note= "A997Q mutation"
                                                                                                                         note= "D993A mutation"
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Pred. No.
                                                                                                                                                                                        mutation'
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RESULT 23
AAW34606
ID AAW34

AAW34606 standard; Protein; 1663 AA

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                                                                                                                                                             This sequence represents a mutated human C3 protein of the invention CC (see AAW34606 for wild type protein). This protein is a protein of the CC invention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, CC fragments and conjugates are used to deplete levels of complement CC pathway proteins (by superactivation until one or more components are CC exhausted), specifically to prevent rejection of foreign matterial CC (particularly a xenograft) but also to prevent complement-mediated CC diseases resulting from (surgical) injury or antibody-antigen interaction CC in autoimmune disease, also to localise and/or amplify endogenous CC complement protein conversion and deposition at a specific site (e.g. a CC virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated lymphocytes in extracted bone marrow. Since (A) is not content to the content of the content of factor B (which is then content of factor B (which is then content of factor B (content of factor B content of factor B content
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Best Local S
Matches 13
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07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; Page -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft
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                                                                                                                                                                                                   consumption of factor B.
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13; Conserv
ITHRIHWESASLL 1319
                                   ITHRIHWESASLL
                                                                                                                                                             1663
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                                                                           Conservative
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96GB-0011896.
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/note=
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                                                                                                                   100.0%;
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                                                                             0
                                                                           Score 70; DB 18;
Pred. No. 0.0069;
Mismatches 0
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                                                                                                                   18;
                                                                                                                 Length 1663;
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AAW34606;

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                                                                                                                                                           This sequence represents the wild type human C3 protein. This protein can be mutated to produce a protein of the invention. The protein of the CC invention is a modified native complement pathway protein (A) that forms CC and conjugates are used to deplete levels of complement pathway proteins (CC and conjugates are used to deplete levels of complement pathway proteins CC (by superactivation until one or more components are exhausted), CC specifically to prevent rejection of foreign material (particularly a CC conversat) injury or antibody-antigen interaction in autoimmune CC from (surgical) injury or antibody-antigen interaction in autoimmune CC disease, also to localise and/or amplify endogenous complement protein CC conversion and deposition at a specific site (e.g. a virus, infected cell CC or tumour, to increase sensitivity to complement-mediated responses; a CC particular application is eliminating any cancer cells left after CC surgical removal of a tumour). Also contemplated is ex vivo treatment, CC especially by passing blood through a matrix containing (A) (this may CC mediators) or killing of leukaemia cells or MHC-mismatched lymphocytes in CC contemplated bone marrow. Since (A) is not inhibited by factor I, it can bind repeatedly to factor B (which is then inactivated), causing CC inactivation of the alternative pathway by consumption of factor B.
                                                                Query Match
Best Local S
Matches 13
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07-MAR-1996;
07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement resistant to down-regulation. especially for preventing graft
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                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1; 123pp; English.
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                                                                  l Similarity
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ITHRIHWESASLL 1319
                           ITHRIHWESASLL
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                                                               100.0%;
llarity 100.0%;
Conservative 0
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96GB-0004865.
96GB-0011896.
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                                                                                 Score 70; DB 18
Pred. No. 0.0069
                                                                                                   DB 18;
                                                                                                 Length 1663;
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RESULT 24 AAW34607

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1 ITHRIHWESASLL 13

Matches Query Match Best Local (

Similarity

100.0%;

Score 70; DB 18; Pred. No. 0.0069; Mismatches

DB 18;

Length 1663; Indels

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Conservative

0;

Sequence

1663 AA;

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This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants, fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement-mediated diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating any cancer cells left after surgical removals of a tumour). Also
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07-MAR-1996;
07-JUN-1996;
                                               contemplated is ex vivo treatment, especially by passing blood through a matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or MHC-mismatched lymphocytes in extracted bone marrow. Since (A) is not inhibited by factor I, it can bind repeatedly to factor B (which is then inactivated), causing inactivation of the alternative pathway by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
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                                   consumption
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96GB-0004865.
96GB-0011896.
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1307

ITHRIHWESASLL 1319

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This sequence represents a mutated human C3 protein of the invention CC (see AAW34606 for wild type protein). This protein is a protein of the complement on the invention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, CC fragments and conjugates are used to deplete levels of complement complement gathway proteins (by superactivation until one or more components are call the pathway proteins (by superactivation until one or more components are CC (particularly a xenograft) but also to prevent complement-mediated CC diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous CC complement protein conversion and deposition at a specific site (e.g. a CC virus, infected cell or tumour, to increase sensitivity to complement mediated responses; a particular application is eliminating CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment, especially by passing blood through a contemplated is ex vivo treatment, especially by passing blood through a matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or CC contemplated lymphocytes in extracted bone marrow. Since (A) is not inactivated), causing inactivation of the alternative pathway by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
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08-JUL-1996;
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07-MAR-1996;
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                                     of factor
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96GB-0004865.
96GB-0011896.
96GB-0014293.
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consumption

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RESULT 26
AAW34609
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This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of the cinvention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants, cf fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement-mediated diseases resulting from (surgical) injury or antibody-antigen interaction cin aucoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating any cancer cells left after surgical removal of a tumour). Also contemplated is ex viru treatment, especially by passing blood through a matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or conference of the contemplate of the
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Matches 13
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07-MAR-1996;
07-JUN-1996;
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100.0%; Pred. No. 0.0069;
tive 0; Mismatches 0;
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RESULT 27
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This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), that variants, fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement mediated diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a virus, infected cell or tumour, to increase sensitivity to
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07-MAR-1996;
07-JUN-1996;
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lation resistant C3 convertase; xenograft rejection; therapy;
t-mediated disease; autoimmune disease; leukaemia cell; tumour;
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                                                                                                                                                                                                                                            etc.
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96GB-0004865.
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Pred. No. 0.0069;
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07-MAR-1996;
07-JUN-1996;
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                                                                                                                                                   Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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96GB-0004865.
96GB-0011896.
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965
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Pred. No. 0.0069;
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This sequence (see AAW34606

represents a mutated human C3 protein of the invention for wild type protein). This protein is a protein of the

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English

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RESULT 29
AAW34612
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Best Local
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19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
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                                                                                                                                                           Misc-difference
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96GB-0004865
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998
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996
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Pred. No. 0.0069;
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RESULT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein. This protein is a protein of the invention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants, fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (patricularly a xenograft) but also to prevent complement-mediated diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous
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                                                                                                                                                                                                 down-regulation resistant C3 convertase; xenograft rejection; complement-mediated disease; autoimmune disease; leukaemia ce
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                              Misc-difference
                                                               Misc-difference
                                                                                               Misc-difference
                                                                                                                                                   Homo
                                                                                                                                                                                   complement-mediated response; MHC-mismatched lymphocyte; mutein
                                                                                                                                                                                                                                     Human; C3 protein; convertase; complement pathway protein;
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                                                                                               Location/Qualifiers
                                                                 1002
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Pred. No. 0.0069;
                                                                               mutation"
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                                                                                                                                                                                                     on; therapy; cell; tumour;
                                                                                                                                                                                                                                        infection;
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"V1005H mutation

WO9732981-A1

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RESULT 31
AAW34614
ID AAW34
AC AAW34
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07-MAR-1996;
07-JUN-1996;
                                                        Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
       Homo sapiens
                                                                                                                                                                                                                                                  Human C3 protein mutant DV-3.
                                                                                                                                                                                                                                                                                                                                  09-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW34614 standard; Protein; 1663 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inactivated), causing consumption of factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-457534/42
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13; Conserv
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96GB-0011896
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Pred. No. 0.0069;
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RESULT 32 AAW34615 ID AAW34

AAW34615 standard; Protein; 1663 AA.

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                                                                                            XEFFFFFFFFFXQXQXGXGXGQQXQXQXQXQXQQQQQQ
                                                                                                                               This sequence represents a mutated human C3 protein of the invention CC (see AAW34606 for wild type protein). This protein is a protein of the crimention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, CC fragments and conjugates are used to deplete levels of complement CC pathway proteins (by superactivation until one or more components are CC exhausted), specifically to prevent rejection of foreign material CC (particularly a xenograft) but also to prevent complement-mediated CC diseases resulting from (surgical) injury or antibody-antigen interaction CC complement protein conversion and deposition at a specific site (e.g. a CC complement protein conversion and deposition at a specific site (e.g. a CC complement-mediated responses; a particular application is eliminating CC complement-mediated responses; a particular application is eliminating CC contemplated is ex vivo treatment, especially by passing blood through a contemplated is ex vivo treatment, especially by passing blood through a content inflammatory mediators) or killing of leukaemia cells or CC content of the content of the alternative pathway by is then constituted by factor I, it can bind repeatedly to factor B (which is then constituted), causing inactivation of the alternative pathway by
                               Matches
                                               Query Match
Best Local
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07-MAR-1996;
07-JUN-1996;
                                                                                            Sequence
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13; Conserv
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                                                                                            1663 AA;
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1035
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                               <u>,</u>
                                              Score 70;
Pred. No.
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                               Mismatches
                                            0.0069;
                                                              BB
                                                           Length 1663;
                               Indels
                               0,
                               Gaps
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19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
                     virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating any cancer cells left after surgical removal of a tumour). Also contemplated is ex vivo treatment, especially by passing blood through a matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or MHC-mismatched lymphocytes in extracted bone marrow. Since (A) is not inhibited by factor I, it can bind repeatedly to factor B (which is then inactivated), causing inactivation of the alternative pathway by
                                                                                                                                                                                                                                                                                                                              fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement-mediated diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
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consumption
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of factor
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96GB-0004865.
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1072
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1073
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This sequence represents a mutated human C3 protein of the invention CC (see AAW34606 for wild type protein). This protein is a protein of the cinvention, and is a modified native complement pathway protein (A) that CC invention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, cf fragments and conjugates are used to deplete levels of complement proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign matterial (particularly a xenograft) but also to prevent complement-mediated cd diseases resulting from (surgical) injury or antibody-antigen interaction cin autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating contemplated is ex vivo treatment, especially by passing blood through a mattir containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or contemplated in the contemplated is ex vivo treatment, especially by passing blood through a mattir containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-1996;
07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                       Example 14; Page -; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-457534/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMUT-) IMUTRAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITHRIHWESASLL 1319
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96GB-0004865.
96GB-0011896.
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100.0%; Pred. No. 0.0069;
tive 0; Mismatches 0;
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34617
                       This sequence represents a mutated human C3 protein of the invention (see AW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants, fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement-mediated complement-mediated
     diseases resulting
                                                                                                                                                                                                                                                       Claim 18; Page -; 123pp; English
                                                                                                                                                                                                                                                                                                                                                      Modified complement pathway protein that forms C3 convertage resistant to down-regulation - used to exhaust the complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Farries
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08-JUL-1996;
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                                                                                                                                                                                                                                                                                                      by super-activation, especially for preventing on, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harrison
                     pecifically to prevent rejection of foreign material a xenograft) but also to prevent complement-mediated
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96GB-0004865.
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Pred. No. 0.0069;
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  injury or antibody-antigen interaction
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Best Local S
Matches 13
                                                                                                                                                                                                                    resistant pathway by
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07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
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                                                                                                                                                                                                              Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMUT-) IMUTRAN LTD
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96GB-0004865.
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Pred. No.
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This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) the invention, and is a modified native complement pathway protein (A) the invention of

Page

123pp;

English

a down-regulation resistant C3 convertase.

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ARBSULT 36
AAW34626
ID AAW34626
AC AAW34
XX APW34
XX O9-AF
XX Humar
XX Humar
XX Homo
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XX Compl
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XX W0973
XX W9973
XX I9-NC
PR 07-MJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                  19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
                                                                    Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        consumption
                                                     pathway by super-activation,
                                                                                                                           WPI; 1997-457534/42
                                                                                                                                                              Farries TC,
                                                                                                                                                                                                                                                                                                                           04-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                 W09732981-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human C3
 Example 17; Page -; 123pp; English
                                                                                                                                                                                                 (IMUT-) IMUTRAN LTD.
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                                                                                                                                                              Harrison
                                                                                                                                                                                                                                 96GB-0024028.
96GB-0004865.
96GB-0011896.
96GB-0014293.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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Pred. No. 0.0069;
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                                                       for
                                                     preventing
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07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                  Human; C3 protein; convertase; complement pathway protein; infectiown-regulation resistant C3 convertase; xenograft rejection; tocomplement-mediated disease; autoimmune disease; leukaemia cell; complement-mediated response; MHC-mismatched lymphocyte; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-APR-1998 (first entry)
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Modified complement pathway protein that forms
                             WPI; 1997-457534/42
                                                             Farries
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                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                            (IMUT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                    sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ITHRIHWESASLL 13
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                                                                                            IMUTRAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein mutant FR-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1667 AA;
                                                             Harrison RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                           96GB-0004865.
96GB-0011896.
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                                                                                                                                                                                                                                                                                                     "wild type D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 70; DB 18; Pred. No. 0.0069;
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                                                                                                                                                                                                                                                                                                        mutated to
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 C3 convertase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1667;
                                                                                                                                                                                                                                                                                                                                                                                                                  cell; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n of the (A) that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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CC This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of the cinvention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, CC pathway proteins (by superactivation until one or more complement c2 pathway proteins (by superactivation until one or more complement c3 pathway proteins (by superactivation until one or more complement c3 pathway proteins (by superactivation until one or more complement c4 pathway proteins (by superactivation until one or more complement c4 pathway proteins (by superactivation of foreign material c4 particularly a xenograft) but also to prevent complement-mediated (C4 particularly a xenograft) but also to prevent complement-mediated (C5 complement protein conversion and deposition at a specific site (e.g. a cy runs, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application; a eliminating c4 any cancer cells left after surgical removal of a tumour). Also contemplated is ex vivo treatment, especially by passing blood through a matrix containing (A) (this may remove additional anabylatetic peptides cand other inflammatory mediators) or killing of leukaemia cells or c5 midbited by factor I, it can bind repeatedly to factor B (which is then can sumption of factor B.
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                         Human; complement; C3f; SBLDI; myocardial infarction; surface enhanced laser description ionisation; intracerebral haemorrhage; congestive heart failure; mass spectroscopy; immunoassay; radioimmunoassay; enzyme-linked immunosorbent assay; ELISA;
               Jackowski G,
                                                                  (MARS/)
                                                                                                                                            30-APR-2001; 2001US-0845715
                                                                                                                                                                            30-APR-2001; 2001US-0845715.
                                                                                                                                                                                                                                             US2002161184-A1
                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                           tluorescent immunoassay.
                                                                                                                                                                                                                                                                                                                                                                                                          Human complement C3f derived peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU08967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU08967 standard; peptide; 11
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                                                                                                              (JACK/) JACKOWSKI G.
                                                                                              (THAT/)
                                                 (VREE/)
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                                                              THATCHER B.
MARSHALL J.
YANTHA J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biopolymer marker, useful in diagnosing disease states including myocardial infarction and intracerebral hemorrhage, comprises compliment C3f fragment with a specified molecular weight -
                               New biopolymer markers useful for indicating one particular disease state such as myocardial infarction, congestive heart failure and intracerebral hemorrhage
Claim 1; Page 30; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; biopolymer marker; myocardial infarction; C3f; syndrome > congestive heart failure; intracerebral haemorrhage; complement
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                                                                    insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic a genes from Drosophila interactions -
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N-PSDB; ABL02720.
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ecification, but was obtained in electronic format directly from ftp.wipo.int/pub/published_pct_sequences.
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1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6. /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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    ITHRIHWESASLL 13
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US-08-793-126-1
US-09-132-271-1
US-09-142-334-22
US-09-252-991A-21635
US-09-252-991A-521635
US-09-252-991A-521635
US-09-252-991A-431
US-09-668-529A-43
US-09-668-529A-43
US-09-668-529A-43
US-09-668-529A-43
US-09-668-529A-29
US-08-311-731A-71
US-08-311-731A-71
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US-08-311-731A-71
US-08-311-731A-71
US-08-311-731A-71
US-08-311-731A-71
US-09-413-814-68
US-09-66-262-3
US-09-66-262-3
US-09-66-262-3
US-09-66-262-3
US-09-67-39-7
US-08-29-567-5
US-08-29-567-5
US-08-453-943-2
US-09-057-121-2
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US-09-134-001C-3977
US-09-252-991A-28288
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7038, Appl
2, Appl
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3977, A
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2, Appli
291, App
71, Appl
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ITHRIHWESASLL 13	100. 100. vative	Application US/087931 849297 ORMATION: HAITISON, Richard TATION: HAITISON, Richard TATION: MODIFIED SEQUENCES: 2 DENCE ADDRESS: BEE: HALE AND DORR LI 60 State Street Boston MA TYPE: Floppy disk R: IBM PC COMPATION: READLALE FORM: TTYPE: PATENTION: READLATION NUMBER: US/08/7 DATE: 07-FEB-1997 DATE: 07-FEB-1997 DATE: 07-FEB-1997 DATE: 07-FEB-1997 DATE: 07-FEB-1997 DATE: 07-FEB-1997 DATE: 07-FEB-1997 DATE: 07-FEB-1997 DATE: 07-FEB-1997 DATE: 07-FEB-1997 DATE: 07-FEB-1997 DATE: 07-FEB-1997 DATE: 07-FEB-1997 DATE: 07-FEB-1997 DATE: 01-FEB-1997 DATE: 0		5542 0 5556 0 5556 0 5556 0 796 0 1201 1 105 1 1
5	0%; Score 70 0%; Pred. No 0; Mismat	Alexa Alexa Timoth HUMAN LP LP LP 1 1 1 1 1 1 1 1 1 1 1 2286.	ALIG	3 US-09-25 3 US-09-04 3 US-09-04 4 US-09-16 4 US-09-19 4 US-09-19 4 US-09-49 4 US-09-49 4 US-09-49 5 US-08-8 7 US-09-25 8 US-09-25 9 US-08-63 2 US-08-63 2 US-08-63 2 US-08-63
	70; DB 2; No. 0.0036 natches	rinder yy C3 PROTEINS a a Version #1.	ALIGNMENTS	252-991A-31968 501-572-1 -040-444-1 -1404-52-7 -252-991A-18995 -107-532A-7065 -107-532A-7065 -491-522-1 -491-522-5 -889-013C-6 -107-532A-3813 -129-13-4 -107-532A-3813 -129-13-4 -107-532A-3813 -129-13-4 -131-2813 -1
	Length; ; 0; Indel	1.30		
	663; 0;			sequence seq
	Gaps 0;			31968 A 1, Appli 7, Appli 7, Appli 118995 A 7065, Ap 7065, Appli 6, Appli 6, Appli 6, Appli 8, Appli 4, Appli 4, Appli 8, Appli 8, Appli 8, Appli 9, Appli 9, Appli 181372, A 281472, A 281472, A 281472, A

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US-09-142-334-22
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US-09-142-334-22
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Patent No. 6221657
                                                                       SOFTWARE: Patentin
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/132,271
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/793,126
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/793,126
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 10286.377
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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APPLICANT: Harrison, Richard Alexander
APPLICANT: Farries, Charles Timothy
TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS
                                                                                                             EARLIER APPLICATION NUMBER: PCT/GB97/00603
EARLIER FILING DATE: 1997-03-04
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                         APPLICANT: Farries, Timothy C.
APPLICANT: Harrison, Richard A.
TITLE OF INVENTION: Down-Regulation Resistant
FILE REFERENCE: 4-30443/A/IMU/PCT
                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/142,334
CURRENT FILING DATE: 1999-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 526-5000 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1663 amino acids
                 TYPE: PRT ORGANISM: Homo sapiens
                                                     ENGTH: 1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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o. 6268485
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22644

LENGTH: 281
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US-09-252-991A-21635
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22644
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US-09-252-991A-22644
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                                                                                                                                                                                                                       SEQ ID NO 21635
LENGTH: 280
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                                                                                                                                                                                                                                                         APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6551795
                                                                                                                                                                             TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                   Local
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                                                                              Similarity 6; Conserv
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NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                            60.0%;
46.2%;
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58.3%;
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Pred. No. 4.2;
                                                                                               Score 42; DB
Pred. No. 18;
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RESULT 6

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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-107-532A-5290
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCCCCUS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                            INFORMATION FOR SEQ ID NO: 5290: SEQUENCE CHARACTERISTICS: LENGTH: 264 amino acids
                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                            NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: CD/RC
                 TOPOLOGY: linear MOLECULE TYPE: protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 TPRIAWSSASML 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 THRIHWESASLL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
8; Conserv
                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02354
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YES
                                                                                                                                      (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD/ROM IS09660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB Pred. No. 43; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
43;
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                                                                                                                                               US-09-107-532A-7038
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US-09-107-532A-7038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATENT NO. 6583275
PATENT NO. 6583275
PATENT NO. 6583276
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
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APPLICANT: Lynn A Doucette-Stamm and David Bush

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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 7038:
SEQUENCE CHARACTERISTICS:
Best Local Similarity
Matches 7; Conserv
                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...329
SEQUENCE DESCRIPTION: SEQ ID NO: 7038:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...264
SEQUENCE DESCRIPTION: SEQ ID NO: 5290:
                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: pri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02354
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7038,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 329 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: GENOME THERAPEUTICS CORPORATION
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09107532A
                                    55.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                        protein
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53.3%;
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4; Mismatches
                                        Score 39; DB
Pred. No. 65;
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                                                                     DB
                                                                     4.
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                                                                     Length 329;
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   Indels
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   Gaps
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2 THRIHWESASLL 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-449-218D-43
                                                                                                                                  US-09-668-529A-43
                                                                                                                                                                             APPLICANT: Van Ness, Jeffrey
APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING BONE
TITLE OF INVENTION: MINERALIZATION
TILE OF INVENTION: MINERALIZATION
TILE REFERENCE: 240083,508D1
CURRENT APPLICATION NUMBER: US/09/668,529A
CURRENT FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 43
LENGTH: 267
TYPE: DET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 43
LENGTH: 267
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6489445
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                  Matches
                                                                                  Best Local Similarity
                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Van Ness, Jeffrey
APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
TITLE OF INVENTION: BONE MINERALIZATION
FILE REFERENCE: 240083.508
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brunkow, Mary E.
APPLICANT: Galas, David J.
APPLICANT: Kovacevich, Brian
APPLICANT: Mulligan, John T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/449,218D CURRENT FILING DATE: 1999-11-24 NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Brunkow, mary E.
APPLICANT: Galas, David J.
APPLICANT: Kovacevich, Brian
APPLICANT: Mulligan, John T.
                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 SHEVHWET 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43, Application US/09449218D
o. 6395511
                              2 THRIHWES 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 THRIHWES 9
                                                                4;
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SHEVHWET 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09668529A
                                                                                                                                                                                                                                                                                                                                                                           Paeper, Bryan W.
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Van Ness, Jeffrey
                                                                  Conservative
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                                                                                Score 37; DB 4;
Pred. No. 1.1e+02;
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                                                              Mismatches
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1.1e+02;
                                                                                              Length 267;
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                                                                Gaps
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RESULT 11

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RESULT 12
US-08-887-997B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-668-037A-43
US-08-887-997B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Van Ness, Jeffrey
APPLICANT: Winkler, David G.
APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING BONE
TITLE OF INVENTION: MINERALIZATION
FILE REFERENCE: 240083,508B4
CURRENT APPLICATION NUMBER: US/09/668,037A
CURRENT FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 43
LENGTH: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brunkow, Mary E
APPLICANT: Galas, David J
APPLICANT: Kovacevich, Br
APPLICANT: Mulligan, John
APPLICANT: Paeper, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43, Application US/09668037A Patent No. 6495736 GENERAL INFORMATION:
                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,997B
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, STEVEN R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: G1 5290
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEPHONE: (617) 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: FOLLET
APPLICANT: DEROBE
                                                                         TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                  TOPOLOGY: line
OLECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cambridge STATE: Marridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 4; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 SHEVHWET 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2, Application US/08887997B
5. 5935852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 THRIHWES 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kovacevich, Brian
Mulligan, John T.
Paeper, Bryan W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Genetics Institute, Inc.
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOLLETTIE, MAXIMILLIAN DEROBERTIS, EDWARD M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                protein
                                                                                                           .7) 42-
) 876-5851
NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IS, EDWARD M.
Mammalian Cerberus-Like Protein &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 4;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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RESULT 14
US-08-311-731A-71
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US-08-311-731A-291
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                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0
Marches 5; Conservative
                                                 Sequence 71, Application US/08311731A
PATENT NO. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
Matches
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SMITH, DOU
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: F
TITLE OF INVENTION: F
TITLE OF INVENTION: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: UZZIV
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
H1.0.
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: STREET: BOSTON MASSAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                     165 HLVHWATANL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 SHEVHWET 161
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                                                                                                                                                                                                                    3 HRIHWESASL 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                     Mycobacterium leprae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.9%;
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Pred. No. 2.2e+02;
3; Mismatches 2;
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1.1e+02;
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                                                                                                                                                                                                                                                      Indels
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US-09-413-814-68
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APPLICANT: Wueller, Joachim
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
LENGTH: 700
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 68, Application US/09413814 Patent No. 6225064
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                     APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cino, Paul M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: 1
ORIGINAL SOURCE
ORGANISM: MY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: YES
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NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 617/720-3500
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 538 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.9%;
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Pred. No. 2.2e+02;
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Best Local Similarity
Matches 6; Conserva
        RESULT 17
US-09-066-262-3
; Sequence 3, Application US/09066262
; Patent No. 5965706
                                                                                                                                                   Query Match
Best Local Similarity
""" hes 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,710
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELECPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
APPLICANT: Streeter, David G.
TITLE OF INVENTION: NEW REGULATOR
TITLE OF INVENTION: TRANSCRIPTION
                                                                                                                                                                                                                                                                           TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                   MEDIA: GELL.
LIBRARY: GELL.
CONE: 202344
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                        LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304
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                                                                                                        20 SHRVTWEGAEV 30
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                                                                                                                                    2 THRIHWESASL 12
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                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                 51.4%;
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                                                                                                                                                                   Mismatches
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Pred. No. 2.
                                                                                                                                                                                   Score 36; DB
Pred. No. 55;
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ZIP: 94304
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RESULT 18
US-08-959-004-10
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                                                                                                                                                                                                                                Sequence 10, Application US/08959004
Patent No. 6197543
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,710
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Goli, Sury
APPLICANT: Streeter,
TITLE OF INVENTION: 1
TITLE OF INVENTION: 7
                                                                          NUMBER OF SEQUENCES: 1
                                                                                                                                        APPLICANT:
                                                                                                         TITLE OF INVENTION: HUMAN VESICLE MEMBRANE PROTEIN-LIKE TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/066,262 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                           ADDRESSEE: Incyte Pharmace
STREET: 3174 Porter Drive
             STATE: CA
                             CITY: Palo Alto
COUNTRY:
                                                                                                                                                                                                                                                                                                                                              20 SHRVTWEGAEV 30
                                                                                                                                                                                                                                                                                                                                                                          THRIHWESASL 12
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USA
                                                                                                                                                                                                                     Hillman, Jennifer L.
                                                                                                                                        Shah, Purvi
Kaser, Matthew
                                                                                                                                                                       Lal, Preeti
                                                                                                                                                                                    Yue, Henry
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                             Incyte Pharmaceuticals, Inc
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Pred. No.
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RESULT 19
US-07-646-537B-2
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US-08-959-004-10
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Sequence 2, App---
No. 5348864
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
            TELEFAX: (609) 921-4526 INFORMATION FOR SEQ ID NO: 2:
                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gaul, Timochy J.
REGISTRATION NUMBER: 33,111
REFERENCE/DOCKET NUMBER: DC1(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 921-5901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: 625 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barbacion TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/959,004 FILING DATE: Herewith CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
LIBRARY: GenBa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 08543-4000
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Brist
STREET: P.O. Box
CITY: Princeton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                        P.O. Box 4000
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Pred. No.
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3.7e+02;
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US-08-299-567-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldinė
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757, 23USWO
FILE REFERENCE: 11757, 23USWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 51.4%;
Best Local Similarity 45.5%;
Matches 5; Conservative
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/214,631
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER FILING DATE: 1997-07-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 60/021,272 EARLIER FILING DATE: 1996-07-05
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION: APPLICANT: Davis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 13
                COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                             APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 57.18; les 4; Conservation
                                                                                                                                                                    STREET: 777 Old
CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                             ADDRESSEE: Regeneron Pharmaceuticals, Inc
STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 844 amino acids
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us/08/299,567
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Pred. No. 2e+02;
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Pred. No. 5e+02;
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REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 2
FELECOMMUNICATION INFORMATION:
FELEPHONE: 914-345-7400
FELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acide
TYPE: -234 amino acide
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Patent No. 5516650
Patent No. 5516600
PARENTAL INFORMATION:
PAPPLICANT: BECKMANN, M. P.
PAPPLICANT: CERRETTI, DOUGLAS P.
PAPPLICANT OF INFORMATION: CYTOKINE THAT BITTED TO THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLICANT OF THE PAPPLIC
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                                                                                                                                                                         PILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
PILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                  TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
PRIOR APPLICATION NUMBER: US 08/114,426
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
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ADDRESSEE: IMMUNEX CORPORATION
                                   SEQUENCE CHARACTERISTICS:
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NAME: Kempler, Gail M.
                                                                                                              TELEPHONE: (200, 10044
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Local Similarity 57.1%;
los 4; Conservative
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TOPOLOGY: unknown
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LENGTH:
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238 amino acids
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Pred. No.
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Query Match
Best Local Similarity
Watches 4; Conserve
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GENERAL INFORMATION:
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Best Local S
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FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/ACENT INFORMATION:
ANAME OFFICE ATTURNEY
ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACENTY ACEN
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COMPUTER: Apple MacIntosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acic
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
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APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: SEESE, KATHRYN
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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5. 5738844
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                                Conservative
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57.1%;
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                             Score 35; DB 1;
Pred. No. 2e+02;
2; Mismatches
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Pred. No. 2e+02;
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                                                                                               DB 1;
                                1; Indels
                                                                                            Length 238;
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                                                                                                                                                             Sequence 2, Application US/09358734
Patent No. 6274117
GENERAL INFORMATION:
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Best Local Similarity
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TELEX: 756822
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
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FILING DATE: 30-AUG-1002
PRIOR APPLICATION NOMBER: US 08/1
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APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF THE APPLICATION NAMES OF 
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple System: Apple S
                                                                            APPLICANT:
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FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
FILING DATE: 20-AUG-
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                           TITLE OF INVENTION:
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APPLICATION NUMBER:
FILING DATE: 03-DEC
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REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
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                                                                 CERRETTI,
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, M. P.
, DOUGLAS P.
CYTOKINE THAT BINDS THE CELL SURFACE
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Pred. No. 2e+02;
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; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3977
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US-09-134-001C-3977
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                                                                                                          NUMBER OF SEQ ID NOS:
SEQ ID NO 3977
LENGTH: 332
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEPLERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
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NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
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FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: US/09/358,734
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NUMBER OF SEQUENCES:
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PRIOR APPLICATION DATA:
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OPERATING SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: Apple SYSTEM: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09134001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (206) 233-0644
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Pred. No. 2e+02;
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2828
LENGTH: 356
TYPE: PRT
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                                                                                                                                                US-09-252-991A-31968
                                                                                                                                                                                   SEQ ID NO 31968
LENGTH: 542
TYPE: PRT
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Best Local
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                                                                                                                                     APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PRIOR PATE: 1998-07-27
RIUNG APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
RUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 50.0%;
Local Similarity 85.7%;
nes 6; Conservative
                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
236 HRLHWAAGQV 245
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                                    3 HRIHWESASL 12
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Pred. No. 3.1e+02;
                                                                                        Score 35;
Pred. No.
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                                                                         Mismatches
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2.8e+02;
                                                                                        DB 4;
4.7e+02;
                                                                                                          Length 542;
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RESULT

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RESULT 30
US-09-040-444-1
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Matches
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                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Koepsell, Hermann
APPLICANT: Grundeman, Dirk
APPLICANT: Gorboulev, Valentin
TITLE OF INVENTION: Transport frotein Which Effects The
TITLE OF INVENTION: Transport Of Cationic Xenobiotics and or Pharmaceuticals,
TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202)408-4000
TELEPAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: TOOTHEY, Kimberlin M
REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 0246
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Koepsell, Hermann
APPLICANT: Grundeman, Dirk
APPLICANT: Grundeman, Dirk
APPLICANT: Grundeman, Dirk
APPLICANT: Grundeman, Dirk
APPLICANT: Grundeman, Dirk
APPLICANT: Grundeman, Dirk
APPLICANT: Koepsell, Hermann
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1300 I St
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                               ZIP: 20005-3315
                                                                                     STATE:
                                                                                                                            ADDRESSEE:
STREET: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner STREET: 1300 I Street, N.W., Suite 700
                                                                COUNTRY:
                                                                                                    CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                424 IPHELHWLNVTL 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                556 amino acids
                                                                                                                            E: Finnegan, Henderson, Farabow, Garrett & Dunner,
1300 I Street, N.W., Suite 700
                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transport protein Which Effects The Transport Of Cationic Xenobiotics and\or Pharmaceuticals, DNA Sequences Encoding It And Their Use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02481.1453-00000
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Pred. No. 4.8e+02;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 556;
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IBM PC compatible SYSTEM: PC-DOS/MS-DOS

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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CO11ge, ALLE M.
APPLICANT: Lagiere, Charles M.
APPLICANT: Prockop, Darwin J.
APPLICANT: Prockop, Charles M.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: O'CONDOY, Steven P
REGISTRATION NUMBER: 41.225
REFERENCE/DOCKET NUMBER: 241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,444
FILING DATE: March 18 1000
                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Abrame, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-0060-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                    TELEPHONE: 650-493-5556
                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                             COMPUTER: IBM CON
OPERATING SYSTEM:
                                 TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
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SYSTEM: Windows
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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US-09-107-532A-7065
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US-09-252-991A-18995
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                                                                                                                                                                                                                                                                                                                                           Sequence 7065, Application.
Sequence 7065, Application.
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
APPLICANT: Lynn A DOUCETC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18995, Application US/09252991A Patent No. 6551795
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CURRENT APPLICATION UMMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 595
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Local Similarity 55.6%;
les 5; Conservative
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
                                                                                                       COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                              ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 HRVHW 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 HRIHWESAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                  CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                      STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                      ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rubenfield et al.

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    452
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Pred. No. 5.1e+02;
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Pred. No. 4.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                          and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 595;
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PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26112
LENGTH: 860
TYPE: PRT
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                                                                                            Sequence 11, Applicate Patent No. 6428998
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPERAL INFORMATION: AUDENFIELD et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/60/074,788
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INFORMATION FOR SEQ ID NO: 7065:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
APPLICANT: Colige, Alain
APPLICANT: Lapiere, Charles M.
APPLICANT: Lapiere, Charles M.
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity es 6; Conserv
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NAME: ATINIEllo, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (788)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...796
SEQUENCE DESCRIPTION: SEQ ID NO: 7065:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113
                                                                                                                                                                                                                                   93 LTHRLSFKOASL 104
                                                                                                                                                                                                                                                                       1 ITHRIHWESASL 12
                                                                                                                                                                                                                                                                                                          Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THRIHWES 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 796 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                     Application US/09491522
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Pred. No. 6.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                          Score 35; DB
Pred. No. 7.4e
4; Mismatches
                                                                                                                                                                                                                                                                                                    . 7.4e+02;
2;
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US-09-491-522-5
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TELEPHONE: 650-493-4935
TELEPAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1205 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6428998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Colige, Alain
APPLICANT: Lapiere, Charles M.
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
     COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FAST-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
                                                                                                                                  COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                             STREET: 1155 Av
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds, LLP STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 HRFHWSRCS 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HRIHWESAS 11
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                                                                                                                                                                                                                                                  1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                     Pennie & Edmonds, LLP
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Pred. No. 1e+03;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8389-0060-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1205;
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RESULT 37
US-08-889-013C-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08889013C Patent No. 5919640
                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: FI 930413
APPLICATION NUMBER: FI 930413
FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 227-94
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1016-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                          TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
               TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,013C
FILING DATE: 07-UUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: TIKKANEN, KA
APPLICANT: FINNE, JUKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100 NOI
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITLE OF INVENTION: STREPTOCOCCUS SUIS ADHESIN PROTEIN AND ITLE OF INVENTION: METHOD FOR PRODUCING IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1211 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                      STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       444 HRFHWSRCS 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 HRIHWESAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIKKANEN, KAARINA
Streptococcus suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                227-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 4;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8389-0060-999
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                                                                                                                                              NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...126

SEQUENCE DESCRIPTION: SEQ ID NO: 3813:
US-09-107-532A-3813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 38
US-09-107-532A-3813
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                                                                        Matches
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3813, Application US/09107532A Patent No. 6583275
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (781)893-5007
TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3813:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 ILHQVHW 25
                                   6 HWESASLL 13
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HWETTSVL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 100 Beaver Street
                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                         ENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                        Conservative
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                                                                                         48.6%; Score 34; DB 4; 62.5%; Pred. No. 1.5e+02;
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57.1%;
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Pred. No. 1.3e+02
                                                                        Mismatches
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                                                                                                           Length 126;
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RESULT 39 US-08-729-103-4

Sequence 4, Application US/08729103 Patent No. 5837841

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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF EEQ ID NOS: 33142
SEQ ID NO 19372
LENGTH: 226
                                                                                                                                                                                                                                                                                                                                    US-09-252-991A-19372; Sequence 19372, Application US/09252991A; Patent No. 6551795
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US-08-729-103-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/729,103
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0138 US
REFERENCE/DOCKET NUMBER: PF-0138 US
TELEPHONE: 415-855-0555
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 48.6%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Boli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN REG PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: 8
TOPOLOGY: linea
MOLECULE TYPE: pe
IMMEDIATE SOURCE:
LIBRARY: GenBan
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 שמא: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenBank
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Pred. No. 2e+02;
1; Mismatches
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Search completed: August 28, 2003, 14:14:56 Job time : 30 secs

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Minimum
Maximum
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Perfect score:
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                                                                                                                                                                                                                                                                                                      Score
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seq length: 2000000000
                 3883399338667700
3883399388
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Match
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Gapop 10.0 , Gapext 0.5
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12:
13:
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[1 /cgn2 6/ptodata/1/pubpaa/USO7]

1 /cgn2 6/ptodata/1/pubpaa/USO5

2 /cgn2 6/ptodata/1/pubpaa/USO5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listing first 45 summaries
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/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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           1661
321
322
322
387
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268
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2-6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
2-6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
2-6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
2-6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
2-6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2-6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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                                                                                                                                                                       0 US-09-846-346-1
US-09-875-519A-22
1 US-09-842-758-41
0 US-09-846-349-1
                          US-09-845-715-1

US-09-845-731-1

US-09-842-758-42

US-10-183-116-45

US-10-183-116-47

US-10-183-116-47

US-10-156-761-12347

US-10-074-475-209

US-10-183-116-79
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                                                                                                                                                                                                                                                 US-09-845-730-1
US-09-846-345-1
                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (without alignments)
31.196 Million cell updates/sec
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Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 22, Appl
Sequence 41, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 42, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 209, App
Sequence 209, App
Sequence 209, Appl
Sequence 209, Appl
Sequence 121, Appl
Sequence 121, Appl
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RESULT 2
US-09-846-345-1
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Matches
GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE
TITLE OF INVENTION: OF 1865 DALTONS
FILE REFERENCE: 2132.045
CURRENT APPLICATION NUMBER: US/09/846,345
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
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APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 1690 DALTONS
FILE REFERENCE: 2132 .042
CURRENT APPLICATION NUMBER: US/09/845,730
CURRENT FILING DATE: 2001-04-30
                                                                                                              Sequence 1, Application US Patent No. US20020161182A1
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Patent No. US20020160532A1
GENERAL INFORMATION:
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SEQ ID NO 22
LENGTH: 1663
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NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version
SEQ ID NO 1
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Best Local (
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PRIOR FILING DATE: 1997-03-04
NUMBER OF SEQ ID NOS: 35
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Best Local Similarity
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CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
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TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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1 ITHRIHWESASLL 13
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; ORGANISM: Homo US-09-842-758-41
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CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/200,158
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,780
PRIOR APPLICATION NUMBER: 60/201,006
PRIOR PILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,006
PRIOR APPLICATION NUMBER: 60/201,006
PRIOR APPLICATION NUMBER: 60/201,007
PRIOR PRILING DATE: 2000-05-01
PRIOR PRILING DATE: 2000-05-01
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SEQ ID NO 41
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PRIOR APPLICATION NUMBER: 60/220,591
PRIOR FILING DATE: 2000-07-25
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PRIOR APPLICATION NUMBER: 60/201,474
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PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,186
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PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,238
PRIOR FILING DATE: 2000-05-01
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                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/232,678
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PRIOR APPLICATION NUMBER: 60/201,508
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TYPE: PRT
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APPLICATION NUMBER: 60/263,217
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Taupier, Raymond J
Grosse, William M
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Padigaru, Muralidhara
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Spytek, Kimberly A
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Zerhusen, Bryan D
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  100.0%; Score 70; DB 11; ilarity 100.0%; Pred. No. 0.0063; Conservative 0; Mismatches 0
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; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-349-1
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US-09-846-349-1
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                                                                                                                                                                                              RESULT 8
Sequence 1, Application US/09845731
Publication No. US20030004307A1
GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: Biopolymer Marker Indicative Of Disease State Having A Molecular
TITLE OF INVENTION: 0f 1211 Daltons
FILE REFERENCE: 2132.029
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
S-09-845-715-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 1348 DALTONS
FILE REFERENCE: 2132.030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09845715 Patent No. US20020161184A1
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Best Local Similarity
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CURRENT FILING DATE: 2001-04-30
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CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
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TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 1449 DALTONS
FILE REFERENCE: 2132.034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1307
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11; Conserv
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llarity 100.0%; Pred. No.
Conservative 0; Mismato
                                                                                                                                                                                                                                                                                                                     Conservative
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100.0%; Pred. No.
tive 0; Mismatc
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0.0016;
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-845-731-1
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; Sequence 42, Application US/09842758
; Publication No. US20030083244A1
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                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/200,158
PRIOR FILLING DATE: 2000-04-26
PRIOR PELLONTION NUMBER: 60/200,613
PRIOR PILLING DATE: 2000-04-28
PRIOR PILLING DATE: 2000-04-28
PRIOR PILLING DATE: 2000-04-28
PRIOR PILLING DATE: 2000-04-28
PRIOR PILLING DATE: 2000-04-29
PRIOR PILLING DATE: 2000-05-01
PRIOR PILLING DATE: 2000-05-01
PRIOR PILLING DATE: 2000-05-01
PRIOR PILLING DATE: 2000-05-01
PRIOR PILLING DATE: 2000-05-01
PRIOR PILLING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,236
PRIOR APPLICATION NUMBER: 60/201,238
PRIOR PILLING DATE: 2000-05-01
PRIOR PILLING DATE: 2000-05-01
PRIOR PILLING DATE: 2000-05-01
PRIOR PILLING DATE: 2000-05-01
PRIOR PILLING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,508
PRIOR FILING DATE: 2000-05-03
PRIOR PPLICATION NUMBER: 60/220,591
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/232,678
PRIOR APPLICATION NUMBER: 60/263,217
PRIOR APPLICATION NUMBER: 60/263,217
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/842,758
CURRENT FILING DATE: 2001-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Edward, Szekeres S
APPLICANT: Alsobrook II, John P
TITLE OF INVENTION: NO. US2003001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Vernet,
                                                                                                                                                  PRIOR FILING DATE: 2000-05-03
                                                                                                                                                                 PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/
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MacDougall, John R
Taupier, Raymond J
Grosse, William M
Edward, Szekeres S
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Gerlach, Valerie
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Burgess, Catherine E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malyankar, Uriel M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zerhusen,
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ilarity 100.0%;
Conservative
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Pred. No.
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0.028;
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; LENGTH: 1661
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-842-758-42
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US-10-183-116-47
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Best Local Similarity
""" hes 6; Conserva
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US-10-183-116-45
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PRIOR FILLING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILLING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILLING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILLING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILLING DATE: 2001-05-04
                                                                                                                                                                                          Sequence 47, Application US/10183116 Publication No. US20030092035A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 321
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NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42
APPLICANT: SIMON,
APPLICANT: Han, Sang-kyou
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE 4C1CP1
CUREENT APPLICATION NUMBER: US/10/183,116
CUREENT APPLICATION 2002-06-26
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Publication No.
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/183,116
CURRENT FILING DATE: 2002-06-26
                                                                                                                                     APPLICANT:
                                                                                                                                                    APPLICANT: Anderson, David J. APPLICANT: Dong, Xinzhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
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                                                                                                           Dong, Xinzhong
Zylka, Mark
Simon, Melvin
                                                                                                                                                                                                                                                                                                                                                            HRIHWESASLL 13
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Zylka, Mark
Simon, Melvin
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76.9%;
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US-10-074-475-209
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                                   Sequence 209, Application US/10074475
Publication No. US20030092898A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
                     APPLICANT:
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
VUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12347
LENGTH: 387
TYPE: PRT
                                                                                                                                                     ; ORGANISM: Streptomyces avermitilis US-10-156-761-12347
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US-10-156-761-12347
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                                                                                              Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12347, Application US/10156761 Publication No. US20030119018A1
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                                                                           Matches
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APPLICANT:
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PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
PRIOR PELICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR TILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 322
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 55.7%;
Local Similarity 54.5%;
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 HRLQWQSLKLL 294
189 VDHRTHWEDWS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 HRIHWESASLL 13
                                  1 ITHRIHWESAS 11
                                                                         Similarity 6; Conserv
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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                                                                         Conservative
                                                                                              55.7%;
54.5%;
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                                                                                              Score 39; DB 15; Length 387; Pred. No. 1.5e+02;
                                                                              Mismatches
                                                                              Indels
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Karra, Kalpana

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RESULT 15
US-10-205-219-121
US-10-205-219-121, Application US/10205219
; Publication No. US20030138803A1
; Publication No. US20030138803A1
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TYPE: PRT
ORGANISM: Mus musculus
US-10-183-116-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapien
US-10-074-475-209
                                                                                                                                                                                                                      Query Match
Best Local
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 209
LENGTH: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 79, Application US/101 Publication No. US20030092035A1
                                                                                                                                                                                                       Matches
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PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
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CURRENT FILING DATE: 2002-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE.4C1CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/074,475
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 60/268,292
PRIOR FILING DATE: 2001-02-13
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APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
TITLE OF INVENTION: Genes and Proteins
FILS REFERENCE: DEX-0313
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/222,344
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les 4; Conserv
                                                                                                                              250 HRLKWQSLKLL 260
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                                                                                                                                                                                                     Similarity 6; Conserv
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Liu, Chenghua
Compos
                                                                                                                                                            HRIHWESASLL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dong, Xinzhong
Zylka, Mark
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Pred. No. 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Vernet, Corine A
APPLICANT: Fernandes, Elma
APPLICANT: Shinkets, Richard A
APPLICANT: Herrman, John L
APPLICANT: Majunder, Kumud
APPLICANT: Mishra, Vishnu
APPLICANT: Mezes, Peter S
APPLICANT: Mezes, Peter S
                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. SEQ ID NO 68
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                        APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115A1el Proteins and Nuclec Acids Encoding
FILS REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: GB 0118354.0 PRIOR FILING DATE: 2001-07-27 NUMBER OF SEQ ID NOS: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/205,219
CURRENT FILING DATE: 2002-07-24
                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
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TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
FILE REFERENCE: WL-A-018200
                                                                                                                                                             LENGTH: 2012
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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APPLICANT: Lee, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 530
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
1702 VTHTVHYQSVS 1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
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o. US20020155115A1
                                   1 ITHRIHWESAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 THRIHWES 9
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                                                                         Conservative
                                                                                         54.3%;
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75.0%;
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                                                                                       Score 38; DB 10;
Pred. No. 9.8e+02;
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Pred. No.
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                                                                                                           Length 2012;
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RESULT 17
US-09-800-198-57
; Sequence 57, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:

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              CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-09-09-07
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666.
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
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Best Local S
Matches 5
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SEQ ID NO 57
LENGTH: 2012
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 35988, Application US/09864761
Patent No. US20020048763A1
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PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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CURRENT FILING DATE: 2001-03-05
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APPLICATION NUMBER: PCT/US01/00662
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5; Conserv
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Majumder, Kumud
Mishra, Vishna
Mezes, Peter S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel, David |
Chen, Wensheng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , David R.
el, David K.
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No.
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9.8e+02;
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-6
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
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PRIOR APPLICATION NUMBER: PCT/US01/00669
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APPLICANT: Penn, Sh
APPLICANT: Rank, D
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Best Local Similarity 45.5
Conservative
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-630
PRIOR APPLICATION NUMBER: US 09/774,203
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N: EXPRESSED IN HBL100, SIGNAL = 0.99

N: EXPRESSED IN HEART, SIGNAL = 0.92

N: EXPRESSED IN LUNG, SIGNAL = 1.9

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.4

N: EXPRESSED IN BRAIN, SIGNAL = 1.2

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

N: EXPRESSED IN BASIA, SIGNAL = 1.1

N: EXPRESSED IN B414336, EVALUE 3.60e+00
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Matches
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/180,312
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CURRENT FILING DATE: 2001-05-23
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/632,366
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APPLICATION NUMBER: US 09/608,408
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APPLICATION NUMBER: US 60/234,687
                                                                                                       APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: PCT/US01/00662
                                        FILING DATE:
                                                                      APPLICATION NUMBER: PCT/US01/00669
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                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-09-27
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US20020048763A1
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: 2001-01-30
NUMBER: PCT/US01/00665
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EST_HUMAN HIT: BE877915.1, EVALUE 1.10e-02
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IN PLACENTA, SIGNAL = 1
IN ADULT LIVER, SIGNAL = 0.9
IN FETAL LIVER, SIGNAL = 0.93
IN BRAIN, SIGNAL = 0.83
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 46114,
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                                                                                                                                                                                                                                                                                                                                                                                              Patent No. US20020048763A1
                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
                                                  PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                   APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
                 PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                            TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-01-29
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PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
                                  PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                           FILE REFERENCE: Aeomica-X-1
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OTHER
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APPLICATION NUMBER: PCT/US01/00666
               FILING DATE:
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Chen, Wensheng
                                                                                                                                                                                                                                                                                                                   Rank, David R.
Hanzel, David K.
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                 2000-09-27
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EXPRESSED
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EXPRESSED IN FETAL
EXPRESSED IN BT474
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IN ADULT LIVER, SIGNAL = 1.7
IN BRAIN, SIGNAL = 2
IN HEART, SIGNAL = 1.9
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE:

2001-01-30

PCT/US01/00664 PCT/US01/00669

APPLICATION NUMBER: PCT/US01/00667

2001-01-3

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APPLICANT: Graff, Jonathon M.
APPLICANT: Muenster, Matthew
ITITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
FILE REFERENCE: A34943 090495.0243
CURRENT APPLICATION NUMBER: US/10/002,631C
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 60/300,309
PRIOR FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 324
SOFTWARE: FastSEQ for Windows Version 4.0
TYPE: PRI
TYPE: PRI
TYPE: PRI
TYPE: PRI
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Sequence 135, Application US/10002631C
Publication No. US20030157486A1
GENERAL INFORMATION:
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Best Local
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LENGTH: 134
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NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: SWISSPROT HIT: Q09312, EVALUE 2.00e+00
FEATURE:
NAME/KEY: UNSURE
LOCATION: (136)...(136)
                                                                          ORGANISM: Mus musculus
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: PCT/US01/00661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/234,687
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Pred. No. 1.1e
0; Mismatches
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1.1e+02;
hes 3;
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RESULT 24
US-10-139-814-12
; Sequence 12, Application US/10139814
; Publication No. US20030134790A1
; GENERAL IMPORMATION:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/089,818B

FILING DATE: June 3, 1998

CLASSIFICATIN: 435

CLASSIFICATIN: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US Patent No. US20020164682A1
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APPLICANT: Langenfeld, John
APPLICANT: Langenfeld, John
TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF
TITLE OF INVENTION: CANCER
FILE REFERENCE: 273/136 Michael J. Wise
CURRENT APPLICATION NUMBER: US/10/139,814
CURRENT FILING DATE: 2002-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
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APPLICANT: Follettie, Maximillian
APPLICANT: DeRobertis, Edward M.
TITLE OF INVENTION: Mammalian Cerberus-Like Protein
TITLE OF INVENTION: Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: LAZAK, STEVEN R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
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87 CambridgePark Drive
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NO: 8:
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85.7%;
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Pred. No.
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Pred. No. 2.1e+02;
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US-10-044-716-12
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US-10-286-152A-52
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Best Local Similarity
Conservation
             Sequence 12, Application US/10044716
Publication No. US20020159986A1
GENERAL INFORMATION:
APPLICANT: LANGENFELD, John
TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS
FILE REFERENCE: 270/070US
CURRENT APPLICATION NUMBER: US/10/044,716
CURRENT FILING DATE: 2002-01-11
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SEQ ID NO 12
LENGTH: 267
TYPE: PRT
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LENGTH: 267
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Publication No. US20030134308A1
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CURRENT FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Bone Morphogenic Proteins (BMP), BMP Receptors and BMP Binding TITLE OF INVENTION: and Their Use in the Diagnosis and Treatment of Glaucoma FILE REFERENCE: 2312 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Alcon Research, APPLICANT: Clark, Abbot F
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RIOR APPLICATION NUMBER: US60/261,252
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LOCATION: (484)...(723)
OTHER INFORMATION: Cysteine knot region
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LOCATION: (361)..(741)
OTHER INFORMATION: DAN
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Local Similarity 50.0%;
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Pred. No. 2.
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Pred. No.
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2.1e+02;
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US-09-089-818B-2
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                 Sequence 2, Application US/09089818B
Patent No. US20020164682A1
GENERAL INFORMATION:
APPLICANT: Follettie, Maximillian
APPLICANT: DeRobertis, Edward M.
TITLE OF INVENTION: Mammalian Cerberus-Like Protein
TITLE OF INVENTION: Compositions
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NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
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Matches 4; Conserv
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CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/213,670
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: US 60/266,046
PRIOR APPLICATION NUMBER: US 60/266,046
PRIOR FILING DATE: 2001-02-01
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SOFTWARE: FastSEQ for
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TYPE: PRT
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APPLICANT: Leviten, Michael W.
TITLE OF INVENTION: TRANSCENIC MICE CONTAINING CERBERUS GENE
TITLE OF INVENTION: DISRUPTIONS
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OTHER INFORMATION: DAN
NAME/KEY: misc feature
LOCATION: (484)..(723)
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LOCATION: (490)..(723)
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NAME/KEY: misc_feature
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 NUMBER OF SEQUENCES:
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Compositions
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CORRESPONDENCE ADDRESS:

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) OTHER INFORMATION: Xaa equals any of the US-10-106-698-4945
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1099-09-29
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR PILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SCETTANDER: DESCRIPTION
                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 4945
LENGTH: 292
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                                   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC FEATURE LOCATION: (201)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC FEATURE
LOCATION: (242)
                                                                                                                                                                FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (25)
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NAME: LAZAR, STEVEN R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
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Local Similarity 50.0%;
hes 4; Conservative
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TOPOLOGY: linear
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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87 CambridgePark Drive
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(617) 876-5851
(70 TD NO: 2:
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Pred. No. 2.2e+02;
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               naturally occurring L-amino acids
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RESULT 31
US-10-139-262-2
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                            Matches
                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/323,580 PRIOR FILING DATE: 2001-09-19
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/325,102 PRIOR FILING DATE: 2001-09-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001/09/26
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les 5; Conserv
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Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
                                                                       LTORVHWAEA 52
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Karen GLATT
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Robert C. BAST, Jr.
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Pred. No. 2.3e+02;
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Pred. No. 2
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Sequence 2, Application US/10139262 Publication No. US20020128459A1 GENERAL INFORMATION:

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RESULT 33
US-09-764-891-4103
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; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-139-262-2
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CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US/09/380,287
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: JP 1997-62259
PRIOR FILING DATE: 1997-02-28
PRIOR APPLICATION NUMBER: JP 1998-62263
PRIOR APPLICATION NUMBER: JP 1998-62263
PRIOR APPLICATION NUMBER: JP 1998-62263
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 42
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PRIOR APPLICATION NUMBER: US/09/380,287A
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: JP 1997-62259
PRIOR FILING DATE: 1997-02-28
PRIOR FILING DATE: 1997-02-28
PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-02-25
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LENGTH: 385
TYPE: PRT
                                                                                  Sequence 4103, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
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Best Local Similarity 41.7%;
Matches 5; Conservative
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                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Oryctolagus cuniculus .10-255-969-2
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APPLICANT: TANAKA, TOSHIHIRO
APPLICANT: TSUKADA, SHUICHI
CURRENT APPLICATION NUMBER: US/09/764,891
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CURRENT FILING DATE: 2002-05-07
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TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
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                                                                                                                                                                                                                                                                                                                                         Similarity 41.7%;
5; Conservation
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Pred. No. 3
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Pred. No. 3e+02;
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Query Match
Best Local Similarity
Matches 6; Conserv:
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US-10-103-313-418
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CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 418
                                                                                                                                                                                                                                                                                             Sequence 541, Application US/10103313 Publication No. US20030082758A1 GENERAL INFORMATION:
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ07C1
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Publication No. US20030082758A1
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                                                             Query Match
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Prior Application removed - See File Wrapper or Palm SOFTWARE: PatentIn Ver. 2.0
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ07C1
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CURRENT FILING DATE: 2002-03-12
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                                                                                                      LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
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                                 Conservative
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66.7%;
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                                Score 37; DB 15;
Pred. No. 3.1e+02;
2; Mismatches 1
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Pred. No. 3.1e+02
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Pred. No. 3.1e+02;
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                                                             Length 390;
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333 ITHNIHYEN 341

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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 130 —
; OTHER INFORMATION: Xaa is Tyr or His or Gln or Asn or Lys or Asp or Glu
US-10-255-969-6
                                                                                                                                                                                                                                                                                    FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/255,969
CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US/09/380,287
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: UP 1997-62259
PRIOR FILING DATE: 1997-02-28
PRIOR FILING DATE: 1997-02-28
PRIOR APPLICATION NUMBER: UP 1998-62263
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 42
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; NAME/KEY: misc_feature
; LOCATION: 130 -
; OTHER INFORMATION: Xaa is Tyr or His or Gln or Asn or Lys or Asp or Glu
US-10-139-262-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-255-969-6
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                                                                                                                                                                             SEQ ID NO 6
LENGTH: 433
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10255969 Publication No. US20030083486A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/10139262 Publication No. US20020128459A1 GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/09/380,287A
PRIOR TILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: JP 1997-6225
PRIOR FILING DATE: 1997-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NAKAMURA, YUSUKE
APPLICANT: TANAKA, TOSHIHIRO
APPLICANT: TSUKADA, SHUICHI
TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/139,262
CURRENT FILING DATE: 2002-05-07
                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver.
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TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NAKAMURA, YUSUKE
APPLICANT: TANAKA, TOSHIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 433
TYPE: PRT
ORGANISM: Mus musculus
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ilarity 41.7%;
Conservative
52.9%;
41.7%;
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; Pred. No. 3.4e
5; Mismatches
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Score 37; DB 15;
Pred. No. 3.4e+02;
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                     Length 433
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                                                                                                            ; ORGANISM: Homo sapiens
US-10-255-969-4
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APPLICANT: NAKAMURA, YUSUKE
APPLICANT: TANAKA, TOSHIHIRO
APPLICANT: TSUKADA, SHUICHI
TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4
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                                    Matches
                                                      Query Match
Best Local
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Publication No. US20030083486A1
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Publication No. US20020128459A1
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ORGANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US/09/380,287A
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: UP 1997-62259
PRIOR FILING DATE: 1997-02-28
PRIOR APPLICATION NUMBER: UP 1998-62263
PRIOR PILING DATE: 1998-62263
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP PRIOR FILING DATE: 1998-02-25 NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US/09/380,287
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: JP 1997-622:
PRIOR FILING DATE: 1997-02-28
                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/255,969
CURRENT FILING DATE: 2002-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAKAMURA, YUSUKE
APPLICANT: TANAKA, TOSHHIRO
APPLICANT: TSUKADA, SHUCHI
TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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CURRENT FILING DATE: 2002-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                 TYPE: PRT
                                                                                                                                                                ENGTH:
                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    410 LSHSLYWEVSSL 421
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1 ITHRIHWESASL 12
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Similarity 41.7%;
5; Conservative
                                  Similarity 41. 5; Conservative
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Pred. No. 3.4e+02;
                                Score 37; DB 15;
Pred. No. 3.4e+02;
5; Mismatches 2;
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                                                                     Length 440
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Sequence 2, Application US/09938330

Ratent No. US20020115838A1

GENERAL INFORMATION:

APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Turner, C. Alexander Jr.

TITLE OF INVENTION: No. US20020115838A1el Human Proteases and Polynucleotides Encodin
FILE REFERENCE: LEX-0237-USA
CURRENT FILLING DATE: 2031-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR PILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 26
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 451
TYPE: PRT
CORGANISM: homo sapiens
Search completed: August 28, 2003, 14:22:54 Job time: 58 secs
                                                                                             В
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US-09-938-330-2
                                                                                                                                                                               Query Match 52.9%;
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                           434 HRFHWSRCSKL 444
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410 LSHSLYWEVSSL 421
                                                                                                                       3 HRIHWESASLL 13
                                                                                                                                                                                 Score 37; DB 10; Length 451; Pred. No. 3.5e+02; 0; Mismatches 5; Indels
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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           AC14U

AC25097

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882597

882523

B867037

B86713

AB132969

T29569

T20894

AC1414

AB1790

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AB1790

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UL9 protein -
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
36	36	36	36	36	36	36	36	36	36	36	36	36	36	37	37
51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4		52.9	52.9
448	426	421	354	348	345	326	320	300	291	261	171	164	147	1456	858
N	_	μ	N	N	N	N	N	N	N	N	N	N	N	N	N
A83775	B71249	S26605	D41080	T21627	JC7681	T49966	S35007	G70943	AI2357	A26344	C70542	S29392	G86749	G86466	T18946
hypothetical prote	hypothetical prote	myb-related protei	probable aldolase	hypothetical prote	septin 3B - human	myb-related protei	nodulation protein	hypothetical prote	hypothetical prote	carbonate dehydrat	hypothetical prote	estradiol-stimulat	conserved hypothet	hypothetical prote	probable phospholi

ALIGNMENTS

Ä;Reference number: A45830; MUID:89309808; PMID:2473125	L9 protein -
A;Title: The difference between human C3F and C3S results from a single amino acid change	ved hypothet etical prote
A;Note: sequence corresponding to residues 1072-1100 was not determined but was taken in R;Poznansky, M.C.; Clissold, P.M.; Lachmann, P.J. I Tempunol 143 1954-1958 1980	n T10022.23 le trna delt etical prote
A; Molecule type: protein A; Residues: 1002-1012, 'E', 1014-1303 <hel></hel>	ved hypothet etical prote
A;Accession: A23435; MOID:00V29442; FMID:30/0031	le PRT1 prot
A;Title: Amino acid sequence of the trypsin-generated C3d fragment from human complement	yndrome cell
R;Hellman, U.; Eggertsen, G.; Engstrom, A.; Sjoquist, J. Biochem. J. 230, 353-361, 1985	etical prote
A; Residues: 1409-1563 <dao></dao>	etical prote
A;Accession: A27603	ved hypothet
A;Title: A 34-amino acid peptide of the third component of complement mediates properdin A;Reference number: A27603; MUID:88154452; PMID:3279119	ansporter re
	ansporter re
A;Resiques: 672-680, N.,682-699, Q.,701-748 <hug> R:Daondaki M.E.: Becherer J.D. IJambris J.D.</hug>	vneurosporen
A; Molecule type: protein	etical cytos
A;Accession: A92187	etical prote
A:Reference number: A92187; MUID:76669169; PMID:2238393	etical prote
J. B101. Chem. 250, 8293-8301, 1975 p. Hittle. Himan anaphiciatricia (Cla) from the third component of complement	rocein - yea
R;Hugli, T.E.	etical prote
A; Note: the authors translated the codon GGT for residue 6 as Leu, CCC for residue 7 as	
A:Cross-references: GB:M63423	ment C3 prec
A; Molecule type: DNA	ption
A;Accession: A37999	•
A;Contents: intron/exon structure of gene	
A: Title: Structural features of the numan C3 gene: intron/exon organization, transcription A: Reference number: A37999: MUID: 91113687: PMID: 1703437	
Biochemistry 30, 1080-1085, 1991	
RyVik, D.P.; Amiquet, P.; Moffat, G.J.; Fey, M.; Amiquet, Barras, F.; Wetsel, R.A.; Tack,	g printed,
A; Residues: 1-1663 < DEB>	9170 9
A;Accession: A94065 A;Molecule type: mRNA	
A; Reference number: A94065; MUID:85140166; PMID:2579379	
Proc. Natl. Acad. SciU.S.A. 82,_708-712,_1985	
C;Accession: A94065; A37999; A92187; A27603; A23435; A45830; B45830; A01257; A01258 R; de Bruijn. M.H.L.; Fey. G.H.	
C;Specites: Homo sapiens (man) C:Date: 28-Nuc-1985 #securace revision 28-Aug-1985 #rext change 08-Dec-2000	
<pre>complement C3 precursor [validated] - human N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit; (</pre>	
C3HU .	
BESTT/₹ 1	

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A;Map position: 19p13.3-19p13.3
A;Map position: 19p13.3-19p13.3
A;Note: contains 41 exons
C;Superfamily: alpha-2-macroglobulin
C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein;
F;1-22/Domain: signal sequence #status predicted <CGs+
F;23-667,Froduct: complement C3 and C3b beta chain #status predicted <CGs+
F;33-667,672-1663/Product: C3b #status predicted <CGB-
F;33-667,749-1663/Product: C3b #status predicted <CGA-
F;672-1663/Product: C3a anaphylatoxin #status predicted <CGB-
F;749-1663/Product: C3b alpha chain #status predicted <CBB-
F;749-1663/Product: C3b alpha predicted <CBB-
F;955-1303/Product: C3d fragment #status predicted <CDS-
F;955-1303/Product: C3d fragment #status predicted <CGB-
F;955-101/Product: C3d fragment #status predicted <CGS-
F;955-101/Product: C3d fragment #status predicted <CGS-
F;102-1103/Product: C3d fragment #status predicted <CGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1424-1457/Region: properdin binding
F;85,939/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;859-816,627-662,693-720,694-727,707-728,873-1513,1101-1158,1358-1489,1389-1458,1506-19
F;748-749/Cleavage site: Arg-Ser (C3 convertase) #status predicted
F;954-955/Cleavage site: Arg-Glu (complement factor I) #status predicted
F;1010-1013/Cross-link: thiolester (Cys-Gln) #status experimental
F;1303-1304/Cleavage site: Arg-Ser (complement factor I) #status predicted
F;1303-1304/Cleavage site: Arg-Ser (complement factor I) #status predicted
F;1303-1304/Cleavage site: Arg-Ser (complement factor I) #status predicted
                                                                                                                                                                                                                                                                                                                                                complement C3 - rabbit (fragment)
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) (
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 15-Dec-1988 #sequence_revision 07-Oct-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Contents: annotation; disulfide bonds
C;Comment: The sequence shown is the C3 fast (C3F) allele, which is found mainly in Cauc
C;Comment: Complement C3 contains two chains, formed by removal of four residues and lin
alternative complement pathways, releases the C3a anaphylatoxin from the amino end of t
rnative-complement-pathway C3/C5 convertase.
C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign pa
e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by pro
C;Comment: The major site of synthesis of this plasma protein is the liver.
                                                                                                                                                                                  C;Accession: A27602

R;Kusano, M.; Chol, N.H.; Tomita, M.; Yamamoto, K.; Migita, S.; Sekiya, T.; Nishimura, S. Immunol. Invest. 15, 365-378, 1986
A;Title: Nucleotide sequence of cDNA and derived amino acid sequence of rabbit complemen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 315, 85-90, 1993
A; Title: Disulfide bridges in human complement component C3b.
A; Reference number: S27041; MUID:93106233; PMID:8416818
                                                                                         A;Reference number: A27602; MUID:87006907; A;Accession: A27602
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A; Residues: 1212-1223 < PO2>
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A;Accession: B45830
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A; Residues: 1212-1215, 'N', 1217-1223
                                            A; Molecule type: mRNA
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A;Cross-references: GDB:119044;
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Matches 13
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1-726 <KUS>
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Pred. No. 0.00065;
; Mismatches 0;
                                                                                                                                          PMID:3019881
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A;Cross-references: GB:M32434; NID:g164862; PIDN:AAA31190.1; PID:g164863 C;Comment: Complement C3 contains two chains, formed by removal of four residues and lin alternative complement pathways, releases the C3a anaphylatoxin from the amino end of tirative-complement-pathway C3/C5 convertage.

C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation. C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign paer classical-complement-pathway C3/C5 convertage. The activity of C3b is regulated by procycomment: The major site of synthesis of this plasma protein is the liver.

C;Superfamily: alpha-2-macroglobulin

C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein;
                                                                               A;Residues: 1-516 <BOR>
A;Residues: 1-516 <BOR>
A;Cross-references: EMBL:275057; NID:g1420374; PID:e252038; PID:g1420375; MIPS:YOR149c A;Experimental source: strain S288C
A;Experimental source: strain S288C
R;Irie, K.; Araki, H.; Oshima, Y.
Mol. Gen. Genet. 225, 257-265, 1991
                                                                                                                                                                                                                                                                                                          C;Accession: S67037; S13750
R;Bordonne, R.; Camasses, A.; Madania, A.; Martin, submitted to the Protein Sequence Database, July 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein PA5194 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: A82997
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A;Title: Mutations in a Saccharomyces cerevisiae host showing A;Reference number: $13750; MUID:91172125; PMID:2005867 A;Accession: $13750
                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-516 <B
                                                                                                                                                                                                                                                          A; Reference number: $67032
A; Accession: $67037
                                                                                                                                                                                                                                                                                                                                                                                               SMP3 protein - yeast (Saccharomyces cerevisiae)
N,Alternate names: protein O3527; protein YOR149c
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul_1996 #sequence_revision 12-Jul-1996 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE004932; GB:AE004091; NID:g9951493; PIDN:AAG08579.1; GSPDB:GN001
A;Experimental source: strain PAO1
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A; Residues: 1-267 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Complete genome sec
A;Reference number: A82950;
A;Accession: A82997
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Similarity 69.2%;
9; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence of Pseudomonas aeruginosa PA01,
so; MUID:20437337; PMID:10984043
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58.3%;
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Pred. No. 1.3;
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Pred. No. 1.4;
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A;Molecule type: DNA
A;Residues: 1-121,'IK',124-162,'G',164-168,'R',170-278,'L',280-516
A;Cross-references: EMBL:X58121; NID:g4497; PIDN:CAA41123.1; PID:g4

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A;Molecule type: DNA
A;Residues: 1-401 <SIM>A;Residues: 1-401 <SIM>A;Residues: GB:AE004080; GB:AE003849; NID:g9107971; PIDN:AAF85520.1; GSPDB:GN001
A;Cross-references: GB:AE004080; GB:AE003849; NID:g9107971; PIDN:AAF85520.1; GSPDB:GN001
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraxo, D.M.; Carrer, H
Briones, M.R.S.; Bueno, M.R.P.; Facincani, A.P.; Ferreira, A.J.S.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
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Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pseudouridine synthase RluA PA3246 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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H83239
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                                                                                                                                                                                                                                                                                                                       A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 bei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical
C;Species: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A82950; A; Accession: H83239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                     R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
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A; Residues: 1-211 <STO>
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A;Cross-references: SGD:S0005675; MIPS:YOR149c
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                                                                                                                                                                                                                                                                                                    A;Accession: E82521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /pothetical protein XF2735 [imported] - Xylella fastidiosa (strain 9a5c)
;Species: Xylella fastidiosa
;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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Best Local
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Similarity 63.6%;
7; Conservation
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#status predicted <TM3>
#status predicted <TM4>
#status predicted <TM5>
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Pred. No. 5.6;
4; Mismatches
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Pred. No.
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K.; Lim,
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        Frohm
Laigz
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A;Access.....
A;Kstatus; preliminary
A;Molecule type: DNA
A;Residues: 1-615 <STO>
A;Cross-references: GB:AE005176; PID:g12723617; PIDN:AAK04804.1; GSPDB:GN00146
A;Cross-references: GB:AE005176; PID:g12723617; PIDN:AAK04804.1; GSPDB:GN00146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Recference number: A86625; MUID:21235186; PMID:11337471
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                                                                                                                                                                                                                                                                                                                   A;Gene: cydC
C;Superfamily: Mycobacterium tuberculosis probable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein cydC [imported] - Lactococcus lactis subsp. lactis (strain IL1403) c;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 24-Aug-2001 C;Accession: B86713
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A;Contents: annotation
                                                                                                                                                                  Matches
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Best Local
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THRLHWLSS
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517
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66.7%;
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45.5%;
                                                                                                                                                                                                    Score 41;
Pred. No.
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Pred. No. 11;
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                                                                                                                                                             Gaps .
                                                                                                                                                                                                                                                                                                                           ATP-binding
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hypothetical cytosolic protein BMEI0303 [imported] - Brucella melitensis (strain C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002 C;Accession: AI3289
                                                                                                                                                                                                                                                                                                                                                             R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesso Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
                                      A;Molecule type: DNA
A;Residues: 1-229 <KUR>
A;Cross_references: GB;AE008917; PIDN:AAL51484.1;
A; Experimental source: strain
                                                                                                                                                                                                                       A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens: A;Reference number: AD3252; PMID:11756688
A;Accession: AI3289
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Status: preliminary

;Map position: I ;Superfamily: Rickettsia

prowazekii hypothetical protein RP073

PID:g17982196;

GSPDB:GN00190

16M)

Query Match Best Local

Local Similarity

57.1%; 58.3%;

Score 40; Pred. No.

DB 14;

2:

Genetics:

BMEI 03 03

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Query Match
Best Local Similarity
"herhes 6; Conserva
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C.Superfamily: Caenorhabditis elegans hypothetical protein C44C1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T29569
R;Bradshaw, H.; Stellyes, L.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C44C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein C44C1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
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    R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Az C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret,
                                                                       C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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A; Accession: T50894
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A;Description: Determination of Nucleotide Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Nagashima,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-259 < BRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: Z20642
A;Accession: T29569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-406 <NAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Rubrivivax gelatinosus;
Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       Experimental source: strain IL144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: T50894
                                                           Accession: C69611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
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                                                                                                                      transporter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6;
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                                                                                                   required for expression of cytochrome llus subtilis
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                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: U41030; PIDN: AAA82366.1; CESP: C44C1.1
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                                                                                                                                                                                                                                                                                                                     55.7%;
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75.0%;
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Pred. No. 16;
                                                                                                                                                                                                                                                                                                                     Score 39;
Pred. No.
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                                                                                 02-Feb-2001
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    ; Azevedo, V
V.; Carter,
ret, C.; Fe
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    Berter
M.; Chd
ri, E.
                                                             RESULT 13
AC1414
ABC transporter required for expression of cytochrome BD homolog cydC [imported] C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
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A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler. iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serorakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Accession: C69611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma. A;Authors: Kreft, U.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Tittle: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding C;Keywords: ATP; nucleotide binding; P-loop F;343-537/Domain: ATP-binding cassette homology <ABC>F;360-367/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                  C; Superfamily: Mycobacterium tuberculosis probable
                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Restdues: 1-574 <GIA>
A;Croost-references: GB:AL592022; PIDN:CAC98090.1; PID:g16415399; GSPDB:GN00178
A;Experimental source: strain Clip11262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-567 < KUN>
A; Cross-references: GB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F. D.; Jones, L.M.; Karst, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABC transporter required for expression of cytochrome
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                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                Genetics:
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527
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                                                                                                                     Similarity 5; Conserv
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                                                          THRIHW 7
                                                                                                                         Conservative
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                                                                                                                                                      55.7%;
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83.3%;
                                                                                                                         1; Mismatches
                                                                                                                                                      Score 39; DB Pred. No. 56;
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                                                                                                                                                                                                                                                     ABC transporter
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Fsihi, H.
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C;Accessio
R;Glaser,
                                                                                                               hypothetical protein Rv1085c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                     Rajandream, M.A.; Rogers, J.; Rutter, Nature 393, 537-544, 1998
                                                       R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N
                                                                                                       C; Accession: C70895
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Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein Atu2746 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1414
                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-228 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43727.1;
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; MUID:21608550; A; Accession: AIZ913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Authors: Yoo, H.; Tao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:NC_003210;
A;Experimental source: strain EGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Molecule type: DNA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          position: circular chromosome srfamily: Rickettsia prowazekii hypothetical
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Sulston, J.E.; Taylor, K.; Whitehead,
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Pred. No. 56;
1; Mismatches
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Pred. No.
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                                    S.; Seeger, K.; Skelton, S.; Squares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Engineer Agrobacterium tumefaciens PMID:11743193
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S.; Barrell, B.G
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Fsihi, H.
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A; Dictuse From A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-242 <COL>
A; Residues: 1-242 <COL>
A; Cross-references: GB:AL021897; GB:AL123456; NID:g3256022; PIDN:CAA17201.1; PID:g289672
 A;Cross-references:
A;Map position: 8R
C;Superfamily: Sacch
                                                                                     A;Molecule type: DNA
A;Residues: 1-280 <LAT>
A;Cross-references: EMBL:U00061; NID:g487943;
                                                                                                                                            submitted to the EMBL Data Library, May 1994 A; Description: The sequence of S. cerevisiae A; Reference number: $46696 A; Accession: $46699
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A;Map position: circular of
C;Superfamily: Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: D97688
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C; Superfamily: hemolysin
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                                                       A;Gene: MIPS:YHR067w
                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                            hypothetical protein YHR067w -
                                                                                                                                                                                                                                                                                                                                   S46699
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A; Residues: 1-266 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 30-Sep-2001 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein AGR C 4981 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                     Alternate names: hypothetical proteir Species: Saccharomyces cerevisiae Date: 28-Oct-1994 #sequence_revision
;Superfamily: Saccharomyces hypothetical protein YHR067w
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                                                                                                                                                                                                                        ;Latreille,
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5; Conserv
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Rickettsia prowazekii hypothetical
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                                      SGD:S0001109
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                                                                                                                                                                                                                                                                                           yeast (Saccharomyces cerevisiae)
1 protein H8025.4
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Pred. No.
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Pred. No.
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33;
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                                                                                       PID:g487947;
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                                                                                         GSPDB:GN00008; MIPS:YHR067w
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Markelz,
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rkelz, B.;
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Query Match

54.3%;

Score

38;

DB

<u>ب</u>

Length 280;

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Down syndrome cell adhesion protein 1 - human (fragment)
N;Alternate names: Down syndrome cell adhesion molecule
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: T08851
R;Yamakawa, K.; Huo, Y.K.; Haendel, M.A.; Hubert, R.; Chen, X.N.; Lyons, G.I
submitted to the EMBL Data Library, September 1997
A;Description: DSCAM: A novel member of the immunoglobulin superfamily maps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, November 1996 A;Reference number: Z19481 A;Accession: T21876
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A; Residues: 1-1896 (YAM)
A; Cross-references: EMBL: AF023449; NID: g3169765; PID: g3169766
A; Cross-references: EMBL: AF023449; NID: g3169765; PID: g3169766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z81533; PIDN:CAB04338.1; GSPDB:GN00023; CESP:F36G9.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-280 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reference number: Z16495
                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
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                                                                                                                                                 5
                                                                                                                                                                  Similarity
                                                                                                               ITHRIHWESAS 11
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                                                                                                                                               Conservative
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                                                                                                                                                                  54.3%;
45.5%;
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1; Mismatches
                                                                                                                                                                  Score 38;
Pred. No.
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A;Cross-references: GB:AE004009; GB:AE003849; NID:G9106980; PIDN:AAF84700.1; GSPDB:GN001
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RESULT 21
S16511
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 03-Jun-2002
C;Accession: AB0500
C;Accession: AB0500
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, R.Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre Nature 413, 523-527, 2001
                                                                      C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: C82625
C;Accession: C82625
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide SequenNature 406, 151-157, 2000
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: C82625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Bruinenberg, P.G.; Evers, M.; Waterham, H.R.; Kuipers, Biochim. Biophys. Acta 1008, 157-167, 1989
A;Title: Cloning and sequencing of the peroxisomal amine A;Reference number: S04963; MUID:89287321; PMID:2500147
A;Accession: S16511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable PRT1 protein - yeast (Pichia angusta)
C;Species: Pichia angusta
C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Genome sequence of Yersinia pestis, the causative A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AB0500
A; Molecule type: DNA
A; Residues: 1-227 <S
                                                                                                                                                                                                                                                                                   conserved hypothetical protein XP1894 [imported] - Xylella fastidiosa (strain C_7Species: Xylella fastidiosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-220 < BRU >
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C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C;Keywords: aminotransferase; intramolecular oxidoreductase; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-609 < KUR>
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                                                A;Status: preliminary
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
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protein T10022.23 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: C86317 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Rifele: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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R;Simpson, A.J.G.; Reinach, F.C.; Camargo, A.A.; Camargo, L.E.A.; Acencio, M.; Alvarenga, R.; Abriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, E. Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrando, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, R.A.; Marqueira, M.B., M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, R.A.; Martins, B.M.F.; Matsukuma, A.Y.; Menok, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; Jeanteili, R.V.; Sawasak A;Authors: da Silva, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santeili, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
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A; Residues: 1-249 <B
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Introns: 109/2
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Pred. No.
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Pred. No. 46;
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                      Local Similarity
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A;Accession: C86317
A,Status: preliminary
A;Molecule type: DNA
A;Residues: 1-280 <STO:
A;Cross-references: GB
                                                                     A; Map position: 2
A; Introns: 120/1; 183/3
C; Superfamily: Canality
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A; Gene: T10022.23
                                                                                                                                                                                   A;Cross-references: EMBL:Z81124; PIDN:CAB03373.1; GSPDB:GN00020; CESP:T21B4.5
A;Experimental source: clone T21B4
                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-341 <WIL>
                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: T25052
                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, October 1996 A;Reference number: Z19974
                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
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C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: F70505
                                                                                                                                                                               A; Experimental source: clone
                                                                                                                                                                                                                                                                      A;Status: preliminary; translated
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A;Residues: 1-314 <COL>
A;Cross-references: GB:Z98209; GB:AL123456; NID:g3261838; PIDN:CAB10903.1; PID:g2292961
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Nature 393, 537-544, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T21B4.5 - Caenorhabditis elegans
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Matches
                                                                                                                                        Gene: CESP:T21B4.5
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nes 5; Conserv
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                                                                     Caenorhabditis hypothetical protein C49G7.2
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    52.9%;
66.7%;
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    Score
Pred.
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Pred. No. 6
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    37;
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DB 72;
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65;
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                         Length 341;
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R;Maekawa, T.; Ohtsubo, E.
Jpn. J. Genet. 69, 269-285, 1994
A;Title: Identification of the region that
A;Reference number: I56963; MUID:94361836;
A;Accession: I76577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-421 <STO>
A;Cross-references: GB:AL450380; NID:g13093060; PIDN:CAC31433.1; GSPDB:GN00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, A;Tile: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; R.; Davies, R.M.; Devlin, K.; Duthoy, S.; leam, M.A.; Rutherford, K.M.
     RESULT
WMBEU9
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                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-698 < RE2 >
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 08-Oct-1999 C;Accession: I60218; I76577; S21899 C;Accession: I60218; I76577; Hughes, G.; Jones, W.A.; McNaughton, J.C.; Stockwell, R;Broom, J.E.; Hill, D.F.; Hughes, G.; Jones, W.A.; McNaughton, J.C.; Stockwell, DNA Seq. 5, 185-189, 1995
A;Title: Sequence of a transposon identified as Tn1000 (gamma delta).
A;Reference number: I60218; MUID:95337425; PMID:7612932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein tnpX - Escherichia coli transposon Tn1000
C,Species: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein ML1052 (imported) -
C;Species: Mycobacterium leprae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: I60218;
A;Accession: I60218
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                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
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                                                                                                                                                                                                                                                                      Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
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Pred. No.
                                                                                                                                                               Score 37; DB 2;
Pred. No. 1.6e+02
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Feltwell, T.;
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Holroyd,
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T18946
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                                                                                                                             A; Introns: 15/3;
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Best Local
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                                                                                          Query Match
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3 HRIHWE--SASLL 13
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A;Cross-references: GB:M19120; NID:g330226; PIDN:AAA45822.1; PID:g330234
R;McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Perry
J. Gen. Virol. 69; 1531-1574, 1988
A;Title: The complete DNA sequence of the long unique region in the genome of herpes simple A;Reference number: A30083; MUID:88274327; PMID:2839594
A;Accession: I28133
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J. Virol. 62, 444-453, 1988
A;Title: Structures of herpes simplex virus type 1 genes required for replication of virualization of virualization of herpes simplex virus type 1 genes required for replication of virualization of herpes simplex virus type 1 genes required for replication of virualization of virualiza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable phospholipase activating protein C05C10.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #Bequence_revision 15-Oct-1999 #text_change 07-Dec-1999 C;Accession: T18946; T24252
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C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000
C;Accession: B29890; I28133
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C;Species: human herpesvirus 1
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A;Experimental source: clone C05C10
                                                                                                                                                                                                                                                                       A; Gene: CESP: C05C10.6
                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z66515; PIDN:CAA91354.1; GSPDB:GN00020; CESP:C05C10.6
A;Experimental source: clone R53
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A; Accession: T24252
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A;Residues: 1-851 <M
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A;Residues: 1-851 <MCG>
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Pred. No. 1.9e
3; Mismatches
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                                           Score 37; DB 2;
Pred. No. 2e+02;
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estradiol-stimulated protein ESP1 - rat (;Species: Rattus norvegicus (Norway rat) C;Date: 25-Feb-1994 #sequence_revision 01-Sep-1995 C;Accession: S29392 R;Nalik, P.; Panayotova-Heiermann, M.; Pongs, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: G86466
R; Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Ansen, N.F.; Hughes, B.; Huizar, L. Mature 408, 816-820, 2000
Rature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein ykcE [imported] - Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Spate: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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A; Residues: 1-147 <STO>
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A;Reference number: A86625; MUID:21235186; PMID:11337471
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                                                                                                                                           RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: hypothetical protein yuiD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE005176; PID:g12723946; PIDN:AAK05097.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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A;Accession: G86466
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Cross-references: GB:AE005172; NID:g5091620; PIDN:AAD39608.1; GSPDB:GN00141
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Species: Arabidopsis thaliana (mouse-ear cress)
spate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
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                                        #text_change 07-May-1999
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A;Status: P-C-A;Status: P-C-A;Residues: 1-82,'G', 83-100,102-261 <RES>A;Residues: 1-82,'G', 83-100,102-261 <RES>
                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-261 <FRA>
R;Fraser, P:; Cummings, P.; Curtis, P.
Mol. Cell. Biol. 9, 3308-3313, 1989
A;Title: The mouse carbonic anhydrase I gene contains two tissue-specific promoters.
A;Reference number: I49573; MUID:90014784; PMID:2571923
                                                                                                                                                                                                                                                                                                                                                                                                                       carbonate dehydratase (EC 4.2.1.1) I - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  x;cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                           R;Fraser, P.J.; Curtis, P.J.
J. Mol. Evol. 23, 294-299, 1986
A;Title: Molecular evolution of the carbonic anhydrase genes:
A;Reference number: A26344; MUID:87169766; PMID:3104601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                       A; Accession: I49573
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A;Experimental source: strain H37Rv
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                                                                                                                                                                                                                                                                                        A; Accession: A26344
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A;Residues: 1-164
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                                                                                               Status: preliminary; translated from GB/EMBL/DDBJ
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Accession: C70542
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¡Species: Mycobacterium tuberculosis
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                             PIDN: AAA50291.1; PID: g556295
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N.; Holroyd,
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hypothetical protein alr4417 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. Strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Accession: A12357
C;Accession: A12357
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, SDNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: A12357
A;Cession: A12357
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A;KStatus: preliminary
A;Molecule type: DNA
A;Residues: 1-291 <KUR>
A;Residues: 1-291 <KUR>
A;COSS-references: GB:BA000019; PIDN:BAB76116.1; PID:g17133553; GSPDB:GN00179
A;COSS-references: Strain PCC 7120
                                                                                                                                                                                                                                                                                    Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 13/1; 79/1; 118/3; 150/3; 171/3; 223/3 C;Superfamily: carbonate dehydratase; carbonic anhydrase C;Keywords: carbon-oxygen lyase; hydro-lyase; zinc F;6-261/Domain: carbonic anhydrase homology <CAH>
                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence r
A;Molecule type: DNA
A;Residues: 1-300 <COL>
A;Cross-references: GB:AL021899; GB:AL123456;
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                   R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: G70943
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Pred. No. 90;
4; Mismatches
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Pred. No. 80;
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Pred. No.
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93;
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septin 3B - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-2001 #sequence
C;Accession: JC7881
R;Methner, A.; Leypoldt, F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: unassigned ATP-binding cassette proteins; C;Keywords: ATP; nucleotide binding; P-loop F;30-221/Domain: ATP-binding cassette homology <ABC>F;47-54/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nodulation protein nodI - Azorhizobium caulinodans
C;Species: Azorhizobium caulinodans
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Feb-2001
C;Accession: S35007
                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 5
A;Introns: 45/1; 88/2; 205/1
C;Superfamily: petunia myb-related protein 1; myb DNA-binding repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myb-related protein-like - Arabidopsis thaliana
N;Alternate names: protein F8M21.200
C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Microbiol. 9, 145-154, 1993
A;Title: Identification of nodSUIJ genes in Nod locus 1 of Azorhizobium caulinodans: evic
A;Reference number: S35006; MUID:94018601; PMID:8412659
A;Accession: S35007
                                                                                                                        RESULT
JC7681
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C;Accession: T49966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: C; Genetics:
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A;Experimental source: cultivar Columbia; BAC clone F8M21
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A; Residues: 1-320 <G
  Biochem. Biophys. Res. Commun.
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A; Accession: T49966
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7; Conservation
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Pred. No. le+02;
2; Mismatches
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Pred. No. 1e+02;
48-56, 2001
                     P.; Lewerenz,
                                                           30-Sep-2001 #text_change
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A;Title: Human septin 3 on chromosome 22q13.2 is upregulated by neuronal differentiation A;Reference number: JC7681; MUID:2122847; PMID:11322766
A;Accession: JC7681
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Maximum Match 100%
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CO3 HUMAN
CO3 RABIT
SMP3 YEAST
RT09 HUMAN
PTXD PSEST
CYDC BACSU
YA85 MYCTU
GEM2 HUMAN
YHM7 YEAST
GLMS WIGBR
GEM2 HUMAN
GLMS WIGBR
RT1 PICAN
MALP3 HUMAN
CAHI MOUSE
CAHI SHEEP
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P00916 macaca mula		O08545 mus musculu					P07720 t genome po			Q9ukw4 homo sapien	P27870 mus musculu

ALIGNMENTS

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STRUCTURE BY NMR OF C3A. MEDLINE=88276894; PubMed=3260670; MEttesheim D.G., Edalji R.P., Mollison K.W., Greer J., Nettesheim D.G., Edalji R.P., Mollison K.W., Greer J.,	SEQUENCE OF 1409-1563. MEDLINE-88154452; PubMed=3279119; Daoudaki M.E., Becherer J.D., Lambris J.D.; "A 34-amino acid peptide of the third component of complement mediates properdin binding."; J. Immunol. 140:1577-1580(1988).	SEQUENCE OF 988-1036. MEDLINE-82174534; PubMed=6175959; Thomas M.L., Janatova J., Gray W.R., Tack B.F.; "Third component of human complement: localization of the internal thiolester bond."; Proc. Natl. Acad. Sci. U.S.A. 79:1054-1058(1982).	SEQUENCE OF 955-966, AND SUBUNITS. TISSUE-Serum; MEDLINE-95293954; PubMed=7539791; Oxvig C., Haaning J., Kristensen L., Wagner J.M., Rubin I., Stigbrand T., Gleich G.J., Sottrup-Jensen L., "Identification of angiotensinogen and complement C3dg as novel proteins binding the proform of eosinophil major basic protein in human pregnancy serum and plasma."; J. Biol. Chem. 270:13645-13651(1995).	SEQUENCE OF 672-748. SEQUENCE OF 672-748. MEDLINE-76069169; PubMed=1238393; Hugli T.E.; "Human anaphylatoxin (C3a) from the third component of complement. "Primary structure."; J. Biol. Chem. 250:8293-8301(1975). [3]	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-85140166; PubMed-2579379; de Bruijn M.H.L.; Fey G.H.; "Human complement component C3: cDNA coding sequence and derived primary structure."; proc. Natl. Acad. Sci. U.S.A. 82:708-712(1985)	LTT 1 HUMAN CO3 HUMAN STANDARD; PRT; 1663 AA. POLOZ4; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Complement C3 precursor [Contains: C3a anaphylatoxin]. C3. C3. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. MCBI TaxID=9606;

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VARIANT GLN-1320.

A Watanabe Y., Matsui N., Yan K., Nishimuana.

A Juji T., Kobayashi N., Kohsaka T.;

XT Matovel C3 allotype C3'F02'has an amino acid substitution that may richibit iC3b synthesis and cause C3-hypocomplementemia.";

RI MOLI Immunol. 30:62-62(193);

CC IMMUNOSI SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL CC COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL CC CAROLLEMENT. SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL CC CAROLLEMENT, VIA ITS RACTIVE COMPLEMENT PATHWAYS.

CC AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE COMPLEMENT C3, CC AFTER ACTIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C3, CC C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89309808; PubMed=2473125; Poznansky M.C., Clissold P.M., Lachmann P.J.; Poznansky M.C., Clissold P.M., Lachmann P.J.; "The difference between human C3F and C3S results from a single ami acid change from an asparagine to an aspartate residue at position 1216 on the alpha-chain of the complement component, C3."; J. Immunol. 143:1254-1258(1989).
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MEDLINE=93106233; PubMed=8416818;
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MEDLINE=90063087; PubMed=2584723;
POZDADANSKY M.C., ClissOld P.M., La
J. Immunol. 143:3860-3862(1989).
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"Disulfide bridges in human
FEBS Lett. 315:85-90(1993).
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BASOPHILIC LEUKOCYTES.
SUBUNIT: C3 precursor is first processed by the removal of 4 Arg residues, forming two chains, beta and alpha, linked by a disulfide bond. C3 convertase activates C3 by cleaving the alpha chain, releasing C3A anaphylatoxin and generating C3B (beta chain)
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Isenman D.E.;
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n complement component C3.";
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C3 secretion.";
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PROSITE; PS00477; ALPHA 2 MACROGLOBULIN; PROSITE; PS01177; ANAPHYLATOXIN_1; 1. PROSITE; PS01178; ANAPHYLATOXIN_2; 1.

Complement pathway; Complement alternate pathway; Plasma; Inflammatory response; Glycoprotein; Signal; Polymorphism

Glycoprotein; Signa cructure; Thioester

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005102; F:receptor binding activity; GO; GO:0007186; P:G-protein coupled receptor GO; GO:0006955; P:immune response; TAS. GO; GO:0007165; P:signal transduction; TAS.
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PDB; 1GHQ; 06-JUN-01.
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**RELEASED.**

**MISCELLANEOUS: I TO FORM C3C AND TO C3C AND T3C T3C.**

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AND A COFACTOR )
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DISEASE: Defects in C3 are the cause of C3 deficiency [MIM:120700], that can result in susceptibility to pyogen infection.
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; PD003264; Anaphylatoxin;
SM00104; ANATO; 1.
SM00643; C345C; 1.
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CO3 RABIT
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01-OCT-1989
15-SEP-2003
 CARBOHYD
SEQUENCE
                           CHAÎN
CROSSLNK
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequence of cDNA and derived amino acid sequence of rabbit complement component C3 alpha-chain.";
Immunol Invest. 15:365-378(1986).

-i- PUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTAGE IS THE CENTRAL REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS. AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES.

-i- SUBUNIT: C3 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 ARG RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE BOND. C3 CONVERTASE ACTIVATES C3 BY CLEAVING THE ALPHA CHAIN, RELEASING C3A ANAPHYLATOXIN & GENERATING C3B (BETA CHAIN + ALPHA)
                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                    InterPro; IPR000020;
InterPro; IPR001599;
InterPro; IPR001134;
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Mammalia; Eutheria;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                               PROSITE; PS01177; ANAPHYLATOXIN_1; PARTIAL. PROSITE; PS01178; ANAPHYLATOXIN_2; PARTIAL. PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
                                                                                                                                                                                                                                                                                             EMBL; M32434; AAA31190.1;
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PF01759; NTR; 1.
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                                                                                                   pathway; Complement alternate pathway; Plasma;
ry response; Glycoprotein; Thioester bond.
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COMPLEMENT C3 ALPHA CHAIN.

1809]ULBAMY] CYSTEINE THIOSETER (CYS-Gln).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

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EMBL; U55020; AAC49635.1; -.
EMBL; 275057; CAA93955.1; -.
PIR; S67037; S67037.
SGD; S0005675; SWP3.
GO; GO:0006276; P:plasmid main
InterPro; IPR005599; PMP.
Pfam; PF03901; PMP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mutations in a Saccharomyces cerevisiae host showing holding stability of the heterologous plasmid pSR1."; Mol. Gen. Genet. 225:257-265(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Wedin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Willing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski m.Y., Skalska U.S., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-leng human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                Koc E.C., Burkhart W., Blackburn K., Moseley A., Sp. "The small subunit of the mammalian mitochondrial identification of the full complement of ribosomal J. Biol. Chem. 276:19363-19374 (2001).
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                                            SEQUENCE
                                                                                                                                                                     Ptam; PF00380; Ribosomal
                                                                                                                                                                                 EMBL; BF034318; -; NOT ANNOTATED CDS.
InterPro; IPR000754; Ribosomal_S9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21276436; PubMed=11279123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
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                                                                                                       Ribosomal
                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                            PD001627; Ribosomal_S9; 1.
; PS00360; RIBOSOMAL_S9; 1.
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                                                                                                       protein;
                                              396
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etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Hominidae; Homo.
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                                              AA;
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                                                                   396
                                                                                                         Mitochondrion;
                                              45822 MW;
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Last annotation update)
S9, mitochondrial precursor (MRP-S9)
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                                          rion; Transit peptide.
MITOCHONDRION (POTENTIAL).
28S RIBOSOMAL PROTEIN S9.
; A4ECC6FD3F7FE9AE CRC64;
      Score
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    Length 396;
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l ribosome:
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28-FEB-2003
                                                                                    Oxidoreductase;
                                                                                                                                                                                                                                                                        EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=316;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- ENZYME REGULATION: Inhibited by NAC1, NADH and sulfite.
-!- INDUCTION: By phosphate starvation.
-!- INDUCTION: By phosphate starvation.
-!- MASS SPECTROMETRY: MM=36413; MM ERR=18; METHOD=MALDI.
-!- MISCELLANEOUS: Its optimum pH is between 7.25 and 7.75
temperature is 35 degrees Celsius.
-!- SIMILARITY: BELONGS TO THE D-ISOMER SPECIFIC 2-HYDROXYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21264507; PubMed=11278981;
Costas A.M.G., White A.K., Metcalf w.W.;
"Purification and characterization of a novel phosphorus-oxidizing
enzyme from Pseudomonas stutzeri WM88.";
J. Biol. Chem. 276;17429-17436(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphonate dehydrogenase (EC 1.20.1.1) (NAD-dependent
                                                                                                 InterPro; IPR006139; 2-Hacid_DH.
InterPro; IPR006140; 2-Hacid_DH_C.
Pfam; PP00389; 2-Hacid_DH; 1.
Pfam; PP02826; 2-Hacid_DH C; 1.
PROSITE; PS00065; D 2 HYDROXYACID_DH_1;
PROSITE; PS00670; D_2_HYDROXYACID_DH_2;
PROSITE; PS00670; D_2_HYDROXYACID_DH_3;
                                                                                                                                                                                                                                                                                                                                                 use by non-profit institu modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                            HSSP; P36234; 1GDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: Catalyzes phosphite (phosphonate)
-!- CATALYTIC ACTIVITY: Phosphonate + NAD(+) + !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular genetic analysis of phosphite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99008986; PubMed=9791102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas stutzeri (Pseudomonas perfectomarina)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas stutzeri WM88.";
Bacteriol. 180:5547-5558(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEHYDROGENASES FAMILY.
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7F55D246CA4454F7 CRC64;
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                                                                                                                                                                                                                         RA Kunst F. (Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Bourilst S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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RA Choi S.K., Codani J.J., Haga K., Funa S., Galizzi A., Galleron N.,
RA Choi S.K., Codani J., Haga K., Haiech J., Bruwood C.R., Henaut A.,
RA Choi S.K., Colaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Krogh S., Kumano M.,
RA Choi S.K., Colaser P., Koningstein G., Krogh S., Kumano M.,
RA Choi S.K., Lauber J., Lazarevic V.,
RA Joris B., Karamata D., Kasahara Y., Klaerr Blanchard M., Nones L.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Repoort G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Viatra B., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RT Subtilia B., Vata K.,
RA Venhamoto K., Yata M.,
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01-NOV-1997
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                                                                                                                  Nature 390:249-256(1997).
-!- FUNCTION: SOMEHOW INVOLVED RESPIRATION. SEEMS TO BE A
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MEDLINE=97124196; PubMed=8969509;
Yoshida K.-I., Shindo K., Sano H.,
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InterPro; IPR003593; AAA, ATPase.
InterPro; IPR001140; ABC_TM_transpt.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00664; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
Problom; PF000006; ABC_transporter; 1.
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15-JUL-1999
15-JUL-1999
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                                                                                                                   MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
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15-JUL-1999 (Rel. 38, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Hypothetical protein Rv1085c.
RV1085C OR MT1117 OR MTV017.38C.
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., I
Peterson J., DeBoy R., Dodson
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
-!- SUBCELLULAR LOCATION: Integral membrane protein (Po
                                                                                       TISSUE-Breast cancer;
MEDLINE-97462902; PubMed-9323129;
Liu Q., Fischer U., Wang F., Dreyfuss G.;
"The spinal muscular atrophy disease gene product, SMN, and associated protein SIP1 are in a complex with spliceosomal
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16-OCT-2001 (Rel. 40, Las
28-FEB-2003 (Rel. 41, Las
Survival of motor neuron
                                                                                                                                                                                                                                                                                                                                   014893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                             NCBI_TaxID=9606
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                   interacting protein 1) (Component of SIP1 OR GEMIN2.
                                                                                                                                                                                                                                                                                                                                                   GEM2
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TubercuList; Rv1085c;
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-!- SIMILARITY: BELONGS TO THE UPF0073 (HLY-III) FAMILY
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InterPro; IPR005744; HylIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for comitties requires a license agreement (See http://www.isb-sib.ch/an
1 90:1013-1021(1997).
1 90:1013-1021(1997).
1 90:1013-1021(1997).
1 FUNCTION: THE SMN COMPLEX PLAYS AN ESSEN SUREN ASSEMBLY IN THE CYTOPLASM AND IS F SPLICING IN THE NUCLEUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
5; Conser
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108 15
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ron protein-interacting
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POTENTIAL.
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Pred. No. 13;
4; Mismatches
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                                          ESSENTIAL ROLE IN
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01-FEB-1995
01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                              MEDLINE=94378003; PubMed=8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dov Johnston M., Andrews S., Brinkman R., Geisel C., Kirsten D. Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Kucaba T., Hillier L., Jier M., Johnston L., Menezes S., McLatreille P., Louis E.J., Macri C., Mardis E., Menezes S., McNahan M., Rikkin L., Rikes L., St Peter H., Trevaskis E., Vaug Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a copyright is produced through a copyright of Bioinformatics and the EMBL the Ewropean Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.
                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Saccharon
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical YHR067W.
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GK; O14893; -.
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                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
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DOMAIN 101 106 POLY-GLN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=S288c / ABS
                                                                                                                                                                                                                                                                                                    "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0005737; C:cytoplasm; TAS.
GO:0005681; C:spliceoseme complex; TAS.
GO:0008248; F:pre-mRNA splicing factor
GO:0006397; P:mRNA processing; TAS.
GO:0000245; P:spliceosome assembly; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: LOCALIZED IN SUBNUCLEAR STRUCTURES COILED BODIES, CALLED GEMS, WHICH ARE HIGHLY ENRICHED IN SPLICEOSOMAL SNRNPS. ALSO FOUND IN THE CYTOPLASM.
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Pred. No. 15;
1; Mismatches
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Akman L.,
Aksoy S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wigglesworthia glossinidia brevipalpis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales.
Enterobacteriaceae; Wigglesworthia.
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15-SEP-2003 (Rel. 42, Last annotation update)
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
(EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GPAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR;
SGD;
                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
SEQUENCE 2
                                                                              TIGRPAMs; TIGRO1135; glmS; 1.
PROSITE; PS00443; GATASE_TYPE_II; 1.
Transferase; Aminotransferase; Glutamine amidotransferase;
                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=22297718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLMS OR WIGBR0110.
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     SEQUENCE
                                                                                                                                 Pfam; PF00310; GATase 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  flies,
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                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate glutamate + D-glucosamine 6-phosphate.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SIS
                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Catalyzes the first step in hexosamine converting fructose-6P into glucosamine-6P using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S46699; S46699.
S0001109; YHR067W.
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5; Conserva
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                                                                  proteome.
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                                                                                                                                                                                                                                                  and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                SUBFAMILY.
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     606
611 AA;
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280 AA;
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ta A., Watanabe H.,
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     68790 MW;
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83.3%;
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BY SIMILARITY.
GLUTAMINE AMIDOTRANSFERASE.
GATASE (BY SIMILARITY).
ISOMERIZATION FRU-6P (BY SIMILARITY).
; 26571D15AF705AAE CRC64;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20289799; PubMed=10830953;
Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
Rosenthal A., Yudoh J., Shibuya K., Kawasaki K., Asakawa S.,
Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.
Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
Lehrach H., Reinhardt R., Yaspo M.-L.,
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                                                                                                                                                                                                                                                                                                                                                                                                             Nature 405:311-319 (2000).

-!- FUNCTION: CELL ADHESION MOLECULE THAT CAN MEDIATE CATION-INDEPENDENT HOMOPHILIC BINDING ACTIVITY. COULD BE INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       060469; 060468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSCAM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intercellular adhesion."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agarwala K.L., Nakamura S., Tsutsumi Y., Yamakawa K.;
"Down syndrome cell adhesion molecule DSCAM mediates homophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyons G.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The DNA sequence of human chromosome
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                                                                                  ISOId=060469-2; Sequence=VSP 002502; VSP_002503; TISSUE SPECIFICITY: PRIMARILY EXPRESSED IN BRAIN. SIMILARITY: Contains 10 immunoglobulin-like C2-type (SIMILARITY: Contains 6 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: TYPE I I SHORT ISOFORM MAY BE SECRETED
                                                                                                                                                                                         Name=Short; Synonyms=CHD2-42
                                                                                                                                                                                                                      Name=Long; Synonyms=CHD2-52;
IsoId=O60469-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                         NERVOUS SYSTEM DEVELOPMENT.
                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genet. 7:227-237(1998).
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                                                                                                                  immunoglobulin-like C2-type domains
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Pred.
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                                                                                                                                                                                                                                                                                                                                                             I MEMBRANE
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Pfam; PF00041; fn3; 6.

Pfam; PF00047; ig; 10.

SMART; SM00060; FN3; 6.

SMART; SM00408; IGc2; 7.

PROSITE; PS50835; IG LIKE; 9.

Immunoglobulin domain; Glycoprotein; Si
Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF023450; AAC17967.1; --
EMBL; AF023449; AAC17966.1; --
EMBL; AF217525; AAF27525.1; --
EMBL; AL163283; CAB90464.1; --
EMBL; AL163283; CAB90436.1; --
EMBL; AL163281; CAB90444.1; --
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InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_cc.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00041; fn3; 6.
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CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 7.

IG-LIKE C2-TYPE 9.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.

FIBRONECTIN TYPE-III 4.

IG-LIKE C2-TYPE 10.

FIBRONECTIN TYPE-III 5.

FIBRONECTIN TYPE-III 6.

BY SIMILARITY.

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28-FEB-2003
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MEDLINE=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague.

Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
GEC 2.6.1.1.6) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase).
GLMS OR YPO4118 OR Y4132.
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"Genome sequence of Yersinia pestis KIM.";

J. Bacteriol. 184:4601-4611(2002).

-!- FUNCTION: Catalyzes the first step in hexosamine metaboli converting fructose-6P into glucosamine-6P using glutamir nitrogen source (By similarity).

-!- CATALYTIC ACTIVITY L. L-glutamine + D-fructose 6-phosphate glutamate + D-glucosamine 6-phosphate.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SISGEPAT SUBPAMILY.
                                                                                                                                                                                                                                    Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., B Perry R.D.;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-KIM5 / Biovar Mediaevalis;
MEDLINE-22137863; PubMed-12142430;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature
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(FTId-VEP 002502.

Missing (In isoform Short).

/FTId-VSP 002503.

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                                                         use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                STRAIN=CBS 4732;
MEDLINE=89287321;
                 EMBL; X15111; CAA33208.1; -. PIR; S16511; S16511.
                                                                                                                                                                                           Hansenula polymorpha.";
Biochim. Biophys. Acta
                                                                                                                                                                                                                                                                                                                           Saccharomycetales;
NCBI_TaxID=4905;
                                                                                                                                                                                                                                                                                                                                                          Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP; MF 00164; -; 1.
InterPro; IPR000583; GATASe 2.
InterPro; IPR001347; SIS.
InterPro; IPR001347; SIS.
                                                                                                                                                                                                                                                     Bruinenberg P.G.,
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     Putative PRT1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P12806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00310; GATase_2; 1. Pfam; PF01380; SIS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; AB0500; AB0500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                   "Cloning and sequencing of the peroxisomal amine oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT1_PICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Aminotransferase; Glutamine amidotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMs; TIGR01135; glms; 1.
PROSITE; PS00443; GATASE_TYPE_II; 1.
                                                                                                                                                                           SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AJ414160; CAC93567.1; -. AE014014; AAM87674.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAHLVHWEQQQGGSLL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITHRIHWE---SASLL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            608 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 12, Created)
(Rel. 12, Last sequence up)
(Rel. 41, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                     Evers M.,
                                                                                                                                                                                            Acta 1008:157-167(1989).
                                                                                                                                                                                                                                                                   PubMed=2500147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
1
603
                                                                                                                                                                                                                                                                                                                                             Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66394 MW;
RNA_rec_mot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%;
                                                                                                                                                                                                                                                    Waterham H.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37.5;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
GLUTAMINE AMIDOTRANSFERASE.
GATASE (BY SIMILARITY).
ISOMERIZATION FRU-6P (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16E5FD0ADB16CCD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                       (See http://www.isb-sib.ch/announce,
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                                                                                                                                                                                                                                                    Kuipers J., Arnberg A.C.,
                                                                                        Usage
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                                                                                Query Match
Best Local (
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FACE.

STRAIN-Sprague-Dawley;

Kallenbach S., La Bella V., Cisterni C., Pettmann B.;

Kallenbach S., La Bella V., Cisterni C., Pettmann B.;

Kallenbach S., La Bella V., Cisterni C., Pettmann B.;

Kallenbach S., La Bella V., Cisterni C., Pettmann B.;

Kallenbach S., La Bella V., Cisterni C., Pettmann B.;

SMN interacting protein-1 expression pattern in rat.";

Submitted (SEP-1990) to the EMBL/GenBank/DBBU databases.

FORMIN THE SMN COMPLEX PLAYS AN ESSENTIAL ROLE IN SPLICEOSOMAL SURVEY ASSEMBLY IN THE CYTOPLASM, AND IS REQUIRED FOR PRE-MRNA SPLICING IN THE CYTOPLASM, AND IS REQUIRED FOR PRE-MRNA SPLICING IN THE CYTOPLASM (BY SIMILARITY).

FORMIN A STABLE HETEROMERIC COMPLEX WITH SURVIVAL OF MOTOR NEITRON PROTEIN (SMN), GENINA AND GEMINA (BY SIMILARITY).

FOR STABLE HETEROMERIC COMPLEX WITH SURVIVAL OF MOTOR NEITRON PROTEIN (SMN), GENINA AND GEMINA (BY SIMILARITY).

FOR STABLE HETEROMERIC COMPLEX WITH SURVIVAL OF MOTOR NEITRON PROTEIN (SMN), GENINA AND GEMINA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09QZP1;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Survival of motor neuron protein-interacting
                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
use by non-profit institutions as lo
modified and this statement is not remo
entities requires a license agreement (
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PROSITE; PS00030; RRM_RNP_1; FALSE_NEGRAL-Dinding.
                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIP1 OR GEMIN2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00360; RRM;
                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEM2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00076; rrm; 1.
                                                                                                                                                      DOMAIN
                                                                                                                                                                                  InterPro; IPR007022; Pfam; PF04938; SIP1;
                                                                                                                                                                                                                     EMBL; AF176072; AAD53287.1; -.
                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116
                                                                                                                                                      processing; Spliceosome; IN 90 95
                                 ω
                                                                Similarity 6; Conserv
                                 HRIHWESASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITHRIHWESASL 12
HRNHWKSQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 AA;
                                                                                                                                   269 AA;
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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24961 MW;
                                                                                                                                   30440 MW;
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                                                                                                                                                                                                                                                                                      institutions as long as atement is not removed. I
                                                                              52.9%;
                                                                                                                                                                                                     SIP1.
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                                                                                                                                                    ; Nuclear protein.
POLY-GLN.
                                                                                   Score 37; DB
Pred. No. 21;
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Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA-BINDING (RRM).
                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                    E03AB9DBFCCC7EE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D317E7EFF49834B5 CRC64;
                                                                  Mismatches
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                                                                                                 DВ
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                                                                                                 ۲,
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(Gemin2).
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                                                                                                   Length 269;
                                                                  Indels
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RESULT 15 MIAA_MYCTU ID MIAA_MYCTU

STANDARD;

PRT;

314

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                                                                                                           Matches
                                                     Query Match
Best Local
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr:
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.",
Nature 393:537-544(1998)."
                                                                                                                                                   HAMAP; MF_00185; -; i.
InterPro; IPR002627; IPPT.
Pfam; PF01715; IPPT; 1.
ProDom; PD004674; IPPT; 1.
TIGRPAMs; TIGR00174; miaA; 1.
Transferase; Nucleotidyltransferase; tRNA processing; ATP-binding;
                                                                                                                                                                                                                                                                                                   EMBL; AE0071(
PIR; F70505;
                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRALN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A.
Fleischmann R.D., Alland D., Gwinn
Reterson J., DeBoy R., Dodson R., Gwinn
Kolonay J.F., Nelson W.C., Umayam L.A.,
Delcher A., Utterback T., Weidman J., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (I
                                                                                                         Complete proteome.

NP_BIND 8

SEQUENCE 314 AA;
                                                                                                                                                                                                                                                                                                                                        EMBL; Z98209; CAB10903.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
-1- FUNCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                        TIGR; MT2799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole genome comparison laboratory strains.";
                                                                                                                                                                                                                                                                    Iubercul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: Isopentenyl diphosphate + tRNA = diphosphate tRNA containing 6-isopentenyladenosine.
SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
FUNCTION: CATALYZES THE FIRST STEP IN THE BIOSYNTHESIS OF
2-METHYLTHIO-NG-(DELTA(2)-ISOPENTENYL)-ADENOSINE (MS[2]I[6]A])
ADJACENT TO THE ANTICODON OF SEVERAL TRNA SPECIES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OR RV2727C OR MT2799
                                                                                                                                                                                                                                                                                                     AE007108; AAK47116.1; -. F70505; F70505.
 w
                                   Similarity
5; Conserv
                                                                                                                                                                                                                                                                ist; Rv2727c; -.
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                                    Conservative
                                                                                                         15 P
34446 MW;
                                                     52.9%;
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                                 Score 37; DB Pred. No. 25; Mismatches
                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis
                                                                                                                        ATP
                                                                                                         DEC948F3569A5513
                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n J.A., Carpenter L., White O., Gwinn M.L., Haft D., Hickey B., L.A., Ermolaeva M.D., Salzberg J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transferase (EC 2.5.1.8) (IPP
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••
                                                                  Length 314;
                                                                                                         CRC64;
                                    Indels
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Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holroyd S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration
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CC. -- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC. -- SIMILARITY: BELONGS TO THE NONASPANIN (TM95F) FAMILY.
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Q9ET30;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42);
15-SEP-2003 (Rel. 42);
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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SEQUENCE
                                   EMBL; AF269150; AAF98159.1; -.
EMBL; AF160213; AAF67014.1, ALT_FRAME.
EMBL; AF116347; AAF22193.1; -.
EMBL; AK000756; BAA91362.1; ALT_INIT.
InterPro; IPR004240; EMP70.
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HUMAN
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                    "NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELIULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: BELONGS TO THE NONASPANIN (TM9SF) FAMILY.
-!- CAUTION: REF 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugasawa T., Lenzen G., Simon S., Hidaka J., Cahen A., Guillaume J. Camoin L., Nahmias C., Strosberg A.D., "The lodocyanopindolol and SM-11044 binding protein (SMBP) belongs the emerging family of MP70 multispanning membrane proteins."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Adrenal gland;
Gu Y., Peng Y., Li Y.,
Wang Y., Chen Z., Fu G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9HD45; Q9NWL8; Q9P0G9; Q9UHW8;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transmembrane 9 superfamily protein member 3
binding protein) (EP70-P-iso)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 128-589 FROM N.A.

Kawakami T., Noguchi S., Itoh T., Shigeta K., Se
Kawakami T., Mizuno T., Morinaga M., Ota T., Suz
Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-1999)
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                      PF02990;
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on of the TM9 super
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suzuki Y., Obayashi N
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RESULT 18
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Best Local
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Q00042;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                  SEQUENCE FROM N.A.
STRAIN=K12 / CR63;
Shimizu H., Saitch Y., Suda Y., Uehara K., Sampei G., Mi
"Complete nuclectide sequence of the F plasmid: its impl
organization and diversification of plasmid genomes.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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CONFLICT
                                                                                                           binding of the transposases encoded by Tn3 and gamma delta to terminal inverted repeat sequences.";
Jpn. J. Genet. 69:269-285(1994).
                                                                                                                                                                                                           MEDLINE=95337425; PubMed=7612932; Broom J.E., Hill D.F., Hughes G., Stockwell P.A., Petersen G.B.;
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      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammar
Enterobacteriaceae; Escherichia.
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6; Conserv
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5:185-189(1995).
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N-LINKED (GLONAC...) (POT
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M -> I (IN REF. 1).
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M -> T (IN REF. 4).
F -> S (IN REF. 4).
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RESULT 19
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P10193;
01-MAR-1989
IRANSFAC; T0095'; -.
InterPro; IPR001410; DEAD.
InterPro; IPR003450; Herpes ori_bp.
InterPro; IPR003450; Herpes ori_bp; 1.
Pfam; PF002399; Herpes_ori_bp; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; DEXDC; 1.
AR ATP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wall modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA su
Alnhaherpesvirinae; Simplexvirus.
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01-MAR-1989 (Rel. 10,
01-OCT-1996 (Rel. 34,
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                                                                                                                                                                                                   EMBL; X14112; CAA32345.1; -.
EMBL; M19120; AAA45822.1; -.
PIR; B29890; WMBEU9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McGeoch D.J., Dalrymple M.A., Dolan A., McNab D., Taylor P., Challberg M.D.; "Structures of herpes simplex virus type 1 genes replication of virus DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=88091053; PubMed=2826807;
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MEDLINE=88274327; PubMed=2839594;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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- FUNCTION: PROBABLY INVOLVED IN DNA REPLICATION. BINDS THE ORIGIN
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SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL9, EHV-1 53, AND VZV 51.
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Best Local S
Matches 5
                                                                                                                                                                                                                                      Colige A., Vandenberghe I., Thiry M., Lambert Li S.-W., Prockop D.J., Lapiere C.M., Nusgens "Cloning and characterization of ADAMTS-14, a high homology with ADAMTS-2 and ADAMTS-3."; J. Biol. Chem. 277:5756-5766 (2002).

-I. FUNCTION: Has a aminoprocollagen type I acactivity in the absence of ADAMTS2. Seems latent enzyme that requires activation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 42, Last annotation update)
15-SBP-2003 (Rel. 42, Last annotation update)
ADAMTS-14 precursor (BC 3.4.24.-) (A disintegrin and metalloproteinase
with thrombospondin motifs 14) (ADAM-TS 14) (ADAM-TS14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AT14 HUMAN STANDARD;
Q8WXS8; Q8TE55; Q8TEY8;
28-FEB-2003 (Rel. 41, Cr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 29-1223 FROM N.A. (ISOFORMS B; C ALTERNATIVE PROMOTER USAGE. MEDLINE=21839041; PubMed=11741898;
                                                                                                                                                                                                                                                                                                                                                                                         "Cloning, expression analysis, and structur: seven novel human ADAMTSs, a family of metadisintegrin and thrombospondin-1 domains."; Gene 283:49-62(2002).
 <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE=21638061; PubMed=11779638;
Bolz H., Ramirez A., von Brederlow B.,
"Characterization of ADAMTS14, a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cal S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fetal lung;
MEDLINE=21856482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochim. Biophys. Acta 1522:221-225(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metalloproteinase family."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                              opez-Otin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADAMTS14.
                                                                                                                                                                                                                latent enzyme that requires actipeptidase activity.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                        matrix (By similarity).
ALTERNATIVE PRODUCTS:
                                     Name=D;
                                                                          Name=C
                                                                                                                                      Event=Alternative
                                                                                                                                                                           Event=Alternative promoter;
                                             Ime=C;
IsoId=Q8WXS8-3; Se
 IsoId=Q8WXS8-4; Sec
Note=Produced by al
ISSUE SPECIFICITY: E
                                                Note=Produced
                                                                                                                                                     alternative
                                                                                                                                                              Comment=2 isoforms, A
                                                                                     IsoId=Q8WXS8-2;
                                                                                                              [soId=Q8WXS8-1;
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                    ion analysis, and structural characterize ADAMTSs, a family of metalloproteinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=11867212;
                                                                                                                                                  promoters;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94261 MW;
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Sequence=VSP_005501;
y alternative splicing
Y: Expressed in retina
                                                Sequence=VSP_006958, VSP_005501; y alternative splicing of isoform
                                                                                                              Sequence=Displayed;
                                                                                     Sequence=VSP_006958
                                                                                                                                      splicing; Named isoforms=4;
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Pred. No.
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oproteinases with
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of the ADAMTS
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Pfam; PF01562; Pep_M12B propep; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF00090; tsp1; 4.
SMART; SM00209; tsp1; 4.
SMART; SM00209; TSP1; 4.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS00546; CYSTEINE SWITCH; FALSE NEG.
PROSITE; PS00427; DISINTEGRIN 1; FALSE NEG.
PROSITE; PS00427; DISINTEGRIN 2; FALSE NEG.
PROSITE; PS50014; DISINTEGRIN 2; FALSE NEG.
PROSITE; PS500142; ZINC PROTEASE; FALSE NEG.
PROSITE; PS500142; ZINC PROTEASE; FALSE NEG.
  CONFLICT
CONFLICT
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DOMAIN
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                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSP1.
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                                                                                VARSPLIC
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                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).

SIMILARITY: Belongs to peptidase family M1
SIMILARITY: Contains 1 disintegrin-like do
SIMILARITY: Contains 1 PLAC domain.
SIMILARITY: Contains 4 TSP type-1 domains.
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AJ345098; CAC87943.1;
AF366351; AAL79814.1;
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253
253
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461
552
730
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968
1063
                                                                                                                                                                                                                                                                                                                                                                  splicing; Alternative promoter usage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor
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1; CAC87943.1; -.
AAL79814.1; -.
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  Α,
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Missing (in isoform B a
/FTId=VSP_006958.
G -> GMCG (in isoform C
/FTId=VSP_005501.
Q -> R (IN REF. 2).
Q -> H (IN REF. 2).
C -> S (IN REF. 2).
C -> Y (IN REF. 2).
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TSP TYPE-1 3.
TSP TYPE-1 4.
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nd isoform C).
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RESULT 21
RMP2_HUMAN
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Expleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Generation and initial analysis of more than 15,000 full-length
T. Generation and mouse 
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                                                               This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formatified and this statement is not removed. Usage by and formatified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McLatchie L.M., Fraser N.J., Main M.J., Wise A., Brown J., Thompson N., Solari R., Lee M.G., Foord S.M.; "RAMPs regulate the transport and ligand specificity of the calcitonin-receptor-like receptor."; Nature 393:333-339(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   060895; QBN1F2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Receptor activity-modifying protein 2 precursor (CRLR activity-modifying-protein 2) (Calcitonin-receptor-like receptor-activity-modifying-protein 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE RAMP FAMILY.
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Primates;
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Pred. No. 1.1e+02;
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entities requires a license agreement (or send an email to license@isb-sib.ch)

(See http://www.isb-sib

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ID CAH1 MOUSE

AC P13634; Q9DC84;

DT 01-FEB-1996 (Rel. 13, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

Tarbonic anhydrase I (EC 4.2.1.1) (Carbonate dehydratase I) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2.1.1) (CA-2
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Best Local
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EMBL; ;
Genew;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Lee N.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006985; RAMP. Pfam; PF04901; RAMP; 1.
                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Spleen; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 "The mouse carbonic anhyd
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90014784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular evolution of the carbonic anhydrase genes: calculation divergence time for mouse carbonic anhydrase I and II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87169766; PubMed=3104601; Fraser P.J., Curtis P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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GO:0005805; C:coated pit; TAS.
GO:0005807; C:integral to plasma membrane; TR
GO:0005764; C:lysosome; TAS.
GO:0015031; P:protein transport; TAS.
GO:0006898; P:receptor mediated endocytosis;
                                                                                                                                                                                                                                                                                                                                                      Cell. Biol. 9:3308-3313(1989)
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BC027975; AAH27975.1;
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6J; TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23:294-299(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=2571923;
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Curtis P.J.;
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Pred. No.
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L -> V (IN REF. 1).
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RECEPTOR ACTIVITY-MODIFYING
EXTRACELLULAR (POTENTIAL).
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      Lee N.H.,
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A Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuller G.D.,

Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Young A.C., Shevchenko Y., Bonffard G.G.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

"Generation and initial analysis of more than 15,000 full-length

"Generation and initial analysis of more than 15,000 full-length

"Generation and initial analysis of more than 15,000 full-length

"Generation and C.S.I. U.S.A. 99:16899-16903 (2002).

"COPACTOR: Reversible hydration of carbon dioxide.

"COPACTOR: Acad. Sci. U.S.A. 99:16899-16903 (2002).

"COPACTOR: Sci. Luc. T. S.A. 199:1689-16903 (2002).

"COPACTOR: Sci. Luc. T. S.A. 199:1689-16903 (2002).

"COPACTOR: Sci. Luc. T. S.A. 199:1689-16903 (2002).

"COPACTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wynshaw-Boris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of
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family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schuler G.D.,
Bhat N.K.,
Heieh F.,
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Mullahy S.J.,
ratne P.H.,
, Hulyk S.W.;
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(See http://www.isb-sib.ch/announce/ a collaboration - MBL outstation -9 9

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EMBL; M32452; AAA37354.1;
EMBL; L36655; AAA50291.1; J
EMBL; M28197; AAA50291.1; J
EMBL; L36650; AAA50291.1; J
EMBL; L36651; AAA50291.1; J
EMBL; L36652; AAA50291.1; J
EMBL; L36653; AAA50291.1; J
EMBL; L36653; AAA50291.1; J
EMBL; L36654; AAA50291.1; J
          METAL
CONFLICT
                                                                                        EMBL;
EMBL;
PIR;
                             METAL
    SEQUENCE
                                    Lyase;
                                          Pfam; PF00194; carb_anhydrase; 1.
Probom; PD00085; Euk COanhd; 1.
PROSITE; PS00152; EUK CO2 ANHYDRASE;
Lyase; Zinc; Metal-binding.
                                                                                  HSSP;
                       METAL
                                                                   MGD; MGI:88268; Carl.
InterPro; IPR001148; Euk_COanhd.
                                    MET
                                                                                       A26344;
                                                                                             L36654; AAA50291.1; JOIN
AK003066; BAB22544.1; -.
BC011223; AAH11223.1; -.
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        BY SIMILARITY.
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S-> P (IN REF. 3
    A0C29A7BBBCFEF0C CRC64;
          (CATALYTIC).
P (IN REF. 3
          AND 4)
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Query Match Best Local Similarity

51.4%; 62.5%;

Score Pred.

No.

ДВ 31;

Length 260;

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RESULT
NODI_AZ
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Q07756;
Q1-OCT-1994
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P48282;
                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Ceta
Bovidae; Caprinae; Ovis.
                                                                                                                                             METAL
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Dorset; TISSUE=Ruminal ep
MEDLINE=96251459; PubMed=8690670
Wang L.Q., Baldwin R.L., Jesse B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHEEP
                                                                                                                                                                    Lyase;
INIT M
                                                                                                                                                                                                                  EMBL; L42178; AAC41634.1; -. HSSP; P00915; 1BZM.
                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                             carbonic anhydrase.";
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ProDom; PD000865; Euk_COanhd; 1.
PROSITE; PS00162; EUK_CO2_ANHYDRASE;
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Pfam; PF00194; carb_anhydrase; 1
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15-SEP-2003
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                                STANDARD;
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                                                                                                                                    28766 MW;
                                                                                                            51.4%;
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sequence update)
annotation updat
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ZINC (CATALYTIC).
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ZINC (CATALYTIC).
; CB96A08F5CB041CE CRC64;
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                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
cora; Bovoidea;
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Best Local S
Matches 7
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Q9UH03;
16-OCT-2001
16-OCT-2001
28-FEB-2003
SEQUENCE FROM N.A. (ISOFORMS A AND B).

Methner A., Lewerenz J., Leypoldt F.;

Methier B., Lewerenz J., Leypoldt F.;

I'Identification and characterization of human septin 3 on chromosome 
"Identification and characterization of human septin 3 on chromosome 
22q13.2 upregulated by retinoic acid induced differentiation of the 
human neuronal precursor cell line Ntera/D2.";

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.

Nodulation; Membrane; ATP-binding; Transport.
NP_BIND 47 54 ATP (BY SIMILARITY)
SEQUENCE 320 AA; 35310 MW; D89B3BF1E7CC4392 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00005; ABC tran; 1.
ProDom; PD00006; ABC transporter; 1.
ProDom; ANA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst. the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                           Homo sapiens (Human).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel.
28-FEB-2003 (Rel.
Neuronal-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Hyphomicrobiaceae; Azorhizobium.
                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                 SEPT3 OR SEP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transpo
Pfam; PF00005; ABC_tran; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Membrane-associated.-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- FUNCTION: FORMS, WITH NODJ, A MEMBRANE IN THE NODULATION PROCESS. IT PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caulinodans: evidence that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94018601; PubMed=8412659;
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l. Microbiol. 9:145-154(1993).
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(Rel. 40, Last sequence update)
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scific septin 3.
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58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36;
Pred. No.
                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D89B3BF1E7CC4392 CRC64;
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RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Bassley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burges J.,
RA Burrill W.D., Button J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
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RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobley V.E., Cole C.G., Cole R.M., Ellington A.G.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Karin J.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.C.T.,
RA Mcclay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.C.T.,
RA Mcclay J., Mashreghi-Mohammadi M., Milne S.A., Mortimore B.J.C.T.,
RA Milliams L., Williams S.A., Williamson H., Wilmes T.E., Wilming L.,
RA Williams L., Williams S.A., Williamson H., Wilmes T.E., Wilming L.,
RA Williams L., Williams S.A., Williamson H., Wilmes T.E., Wilming L.,
RA Williams L., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Williams L., Chaptre J., Becke S., Rogers J., Shimizu N.,
RA Kinsun J., Ewis S., Lin S.-P., Loh P., Malaj B., Nguyen T., Pan H.,
RA Mang O., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakwa S., Kudoh J.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakwa S., Kudoh J.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakwa S., Kudoh J.,
RA Minoshima S., Kawasaki W., Milsen R., Wilming T.,
RA Mcle
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Clamp M., Smink L.J
Bagguley C., Bailey
Bird C.P., Blakey S
                                                                                                                                                                                                  use by non-profit institute. There are no restrictions modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anorsend an email to license@isb-sib.ch).
                                                                                                                            EMBL; AF285107; AAG00517.1; -.
EMBL; AF285109; AAG00519.1; -.
EMBL; Z99716; CAB41235.2; ALT_SEQ.
PIR; JC7681; JC7681.
                                                                Genew; HGNC:10750; SEPT3.
GO; GO:0016288; P:cytokinesis; NAS
InterPro; IPR000038; GTP_Cell_Div.
                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The DNA sequence of human chromosome Nature 402:489-495(1999).
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Tilahun Y., Wright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20057165;
                             Pfam; PF00735; GTP
ProDom; PD002565; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: INVOLVED IN CYTOKINESIS (POTENTIAL).
SUBUNIT: MAY ASSEMBLE INTO A MULTICOMPONENT STRUCTURE
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative
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        division;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9UH03-1; Sequence=Displayed;
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Almeida J.P., Babbage A.
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Interpro; IPRO06771; K bp aldolase.

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Probom; PD002376; K bp aldolase; 1.

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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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28-FEB-2003 (Rel. 41, Last annotation update)
Fructose-bisphosphate aldolase II (EC 4.1.2.13).
                                                                                                 SEQUENCE
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PATHWAY: PART OF REDUCTIVE PENTOSE PHOSPHATE PATHWAY OR CALVIN CYCLE OF PHOTOSYNTHETIC CARBON DIOXIDE ASSIMILATION.
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Neuronal-specific s
SEPT3 OR SEP3.
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Kaneko T., Sato S., Kotani H., Tanaka
Miyajima N., Hirosawa M., Sugiura M.,
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or send a
                                                                                                                                                                                       Synechocystis sp. (strain Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                        Gamma-glutamyltranspeptidase precursor GGT OR SLR1269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Promoter-trap insertion into a novel mammalian septin g during mouse neuronal development.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                  01-NOV-1997
16-OCT-2001
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                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: INVOLVED IN CYTOKINESIS (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kiong J.-W., Stuhlmann H.;
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Sciurognathi; Muridae;
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Asamizu E., Naka
amoto S., Kimura
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                                Nakamura Y.,
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                       MEDLINE=96121379; PubMed=8575760;
Vyas P., Vickers M.A., Picketts D.J., Higgs D.;
"Conservation of position and sequence of a nove
gene containing the major human alpha-globin reg
Genomics 29:679-689(1995).
                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: (5-L-glutamyl)-peptide + an amino acid = peptide + 5-L-glutamyl-amino acid.
-!- PATHWAY: GGT PLAYS A KEY ROLE IN THE GAMMA-GLUTAMYL CYCLE, A PATHWAY FOR THE SYNTHESIS AND DEGRADATION OF GLUTATHONE.
-!- SUBUNIT: THIS ENZYME CONSISTS OF TWO POLYPEPTIDE CHAINS, WHIC SYNTHESIZED IN PRECURSOR FORM FROM A SINGLE POLYPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamada M., Yasuda M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the Synechocystis sp. strain PCC6803. II. Sequence and assignment of potential protein-coding regions.",
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                        CGTHBA
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PROSITE; PS00462; G_GLU_TRANSPEPTIDASE; FALSE_NEG
Transferase; Acyltransferase; Zymogen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                             SEQUENCE
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                         Homo sapiens
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PRINTS; PR01210; GGTRANSPTASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Res. 3:109-136(1996).
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                                                                                                                                                                                                                                   protein (-14 gene protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518 AA;
                             1-62 FROM N.A.
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Shimpo S., Takeuchi C.,
                                                                                                                                                                                                         (Human)
                                                                                                                                                                                                                                                                                                             STANDARD;
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Primates;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAMMA-GLUTAMYLTRANSFERASE SMALL SIMILARITY).
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Wada T., Watanabe i
                                                                                                                                                                                                                                                                   update)
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                                                                                                                                                                                                                                                    update)
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Best Local
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                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S., Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.; "50 million years of genomic stasis in endosymbiotic bacteria."; Science 296:2376-2379(2002).

-!- FUNCTION: Catalyzes the first step in hexosamine metabolism,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
EMBL; AE014078; AAM67598.1; -. HAMAP; MF 00164; -; 1. InterPro; IPR000583; GAMISE_2. InterPro; IPR001347; SIS.
                                                                                                                                                         entities roor send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=22084549; PubMed=12089438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amidotransferase) (Glucosamine-6-phosphate synthase).
GLMS OR BUSG027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glucosamine -- fructose-6-phosphate aminotransferase [isomerizing]
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28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                converting fructose-6P into glucosamine-6P using gnitrogen source (By similarity).

CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phoglutamate + D-glucosamine 6-phosphate.

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: Widely expressed.
SIMILARITY: BELONGS TO THE UPF0171 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 1 type-2 glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                      equires a license agreement (Semail to license@isb-sib.ch).
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(Rel. 41,
(Rel. 41,
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Best Local S
Matches 5
HAMAP; MF_00164; -; 1.
InterPro; IPR000583; GATase_2.
InterPro; IPR005855; GImS.
InterPro; IPR001347; SIS.
Pfam; PF00310; GATase_2; 1.
Pfam; PF01380; SIS; 2.
                                                                                                                                                                                                                                                                                                  MEDLINE-20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
Nature 407:81-86(2000).
-!- FUNCTION: CATALYZES THE FIRST STEP IN HEXOSAMINE METABOLISM,
CONVERTING FRUCTOSE-6P INTO GLUCOSAMINE-6P USING GLUTAMINE AS
NITROGEN SOURCE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-
glutamate + D-glucosamine 6-phosphate.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SIS FAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
(EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GPAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase).
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                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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PROSITE; PS00443; GATASE_TYPE_II; 1.
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Pfam; PF01380; SIS; 2
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GLUTAMINE AMIDOTRANSFERASE.
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GATASE (BY SIMILARITY).
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RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corrby N.R.,
RA Clulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Frasgr A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Frasgr A., French L., Garner P.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLlay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Phillimore B.J.C.T., Patel R., Pearce T.A.V., Peck A.I.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Wilnes J.., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Wiltehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Milnes J.., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Milnes J.., Waray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; "Prediction of the coding sequences of unidentified human genes. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced analysis of CDNA clones from cell line KG-1 and brain."; DNA Res. 3:321-329(1996).
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                NA sequence and comparative analysis of human chromosome
414:865-871(2001).
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Seki N., Ishikawa K.-I
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"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"."

"Generation Acad. Sci. U.S.A. 99:16899-16903(2002).

"Indianal Republication of THE NONASPANIN (TM9SF) FAMILY.

"SMCELLULAR LOCATION: Integral membrane protein (Probable).
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√_RAT
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P54100;
01-OCT-1996
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                             Rattus norvegicus (Rat).
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Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rat
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PROSITE; PS50003; PH_DOMAIN; 1.

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                       PRINTS; PRO0452; SH3DOMAIN.
PRINTS; PRO0452; SH3DOMAIN.
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PRODOM; PD001527; CH type; 1.
ProDom; PD001527; CH type; 1.
ProDom; PD000066; SH3; 1.
SMART; SM00109; C1; 1.
SMART; SM00033; CH; 1.
SMART; SM00033; CH; 1.
SMART; SM000325; RhoGEF; 1.
SMART; SM00252; RhoGEF; 1.
SMART; SM00325; CH; 1.
SMART; SM00326; SH3; 2.
PROSITE; PS50017; DAG PE BIND DO PROSITE; PS50017; DAG PE BIND DO PROSITE; PS50010; DH 2; 1.
PROSITE; PS50010; DH 2; 1.
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Pfam; PF00130; DAG PE-bind; 1
Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGEF; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 2.
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InterPro; IPR003247; CH type.
InterPro; IPR003247; DAG PB-bind.
InterPro; IPR001331; GDS-CDC24.
InterPro; IPR001849; PH.
InterPro; IPR000219; RhoGEF.
InterPro; IPR000980; SH2.
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InterPro; IPR003096; SM22_calponin.
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HSSP; P29354; 1GRI.
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"Tyrosine phosphorylation of Vav stimulates IL-6 cells by a Rac/c-Jun N-terminal kinase-dependent J. Immunol. 163:802-810(1999).
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SIMILARITY: Contains 1 calponin-homology (CH) domain.
SIMILARITY: Contains 1 DBL-homology (DH) domain.
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SUBUNIT: Interacts with SLA (By similarity).
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                  PHORBOL-ESTER AND DAG BINDING
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                                                                                                                  SH2 domain; SH3 domain; Phosphorylation.
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P27870;
01-AUG-1992
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MEDLLINE=91172176; Pubmed=2005887;

Katzav S., Cleveland J.L., Heslop H.E., Pulido D.;

"Loss of the amino-terminal helix-loop-helix domain oncogene activates its transforming potential.";

Mol. Cell. Biol. 11:1912-1920(1991).
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SEQUENCE
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                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92228488; PubMed=1565462;
Adams J.A., Houston H., Allen J., Lints T., Harvey R
"The hematopoietically expressed vav proto-oncogene
with the dbl GDP-GTP exchange factor, the bor gene a
(CDC24) involved in cytoskeletal organization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20130290; PubMed=10662792;
Sosinowski T., Pandey A., Dixit V.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vav proto-oncogene VAV1 OR VAV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oncogene 7:611-618(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Src-like adaptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH SLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-SEP-2003
                                                                                                                                                                                                  FUNCTION: Couples tyrosine kinase the Rho/Rac GTPases, thus leading
                                                                                                                                                                                                                                                                                                                                                                      not in other cell types.
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(Rel. 42, Last ann
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SH2.
SH3 2.
C4A5CACD45FCB80E (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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to cell
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EMBL; X64361; CAA45713.1;

A61187; 1F5X; 1

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M59833;

AAA63402.1;

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Best Local S
Matches 5
     "3_HUMAN STANDARD;
VAV3_HUMAN STANDARD;
Q9UKW4; O95230; Q9Y5X8;
16-OCT-2001 (Rel. 40, Cre
16-OCT-2001 (Rel. 40, Las
28-FEB-2003 (Rel. 41, Las
                                                                                                                                                                                                                                                                           PROSITE; PS50021; CH; 1.

PROSITE; PS00479; DAG PE BIND DOM 1; 1.

PROSITE; PS50001; DAG PE BIND DOM 2; 1.

PROSITE; PS50010; DH 2; 1.

PROSITE; PS500741; DH 1; 1.

PROSITE; PS50003; PH DOMAIN; 1.

PROSITE; PS50001; SH3; 1.

PROSITE; PS50002; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 2.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00888; SM22CALPONIN.
PRODom; PD001527; CH type; 1.
ProDom; PD001093; SH3; 1.
ProDom; PD000066; SH3; 1.
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CONFLICT
SEQUENCE
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SMART; S
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DOMAIN
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DOMAIN
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SMART;
SMART;
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Pfam; PF00130; DAG PE-bind; 1.
Pfam; PF00169; PH; 1.
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                                                                                                                                                                                                                                                           Suanine-nucleotide
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InterPro; IPR001452;
InterPro; IPR003096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001715; Calponin-like.
InterPro; IPR003247; CH_type.
InterPro; IPR003219; DAG PE-bind.
InterPro; IPR001331; GDS CDC24.
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                                                                                                                                                                                                                                                                                                                                                   ; SM00109; C1; 1.
; SM00033; CH; 1.
; SM00233; PH; 1.
; SM00325; RhOGEF; 1.
; SM00326; SH2; 1.
; SM00326; SH3; 2.
protein.
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                                                                                         20
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                                                                                                                           Similarity 5; Conserv
                                                                                        SHRVTWEGAQV 30
                                                                                                          THRIHWESASL 12
                                                                                                                                                                 845
                                                                                                                            Conservative
                                            STANDARD;
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SM22CALPONIN.
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373
504
564
660
765
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Last
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DH.
PH.
PH.
SH3 1.
SH2.
SH3 2.
SH3 2.
SH3 2.
SH3 2.
SH3 2.
SH3 CRC64;
        annotation
               sequence update)
                                                                                                                         Score 36; DB 1; Len
Pred. No. 1.1e+02;
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                                            847
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                                                                                                                                                                                                                                                         SH2 domain; SH3 domain; Phosphorylation;
                                                                                                                                            Length 845;
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GO; GO:0005096; F:GTPase activator activity; TAS.
GO; GO:0005070; F:SH3/SH2 adaptor protein activity; TAS
GO; GO:0007264; P:SH3/SH2 adaptor protein activity; TAS
GO; GO:0007264; P:small GTPase mediated signal transduc
InterPro; IPR001715; Calponin-like.
InterPro; IPR003247; CH type.
InterPro; IPR003219; DAG PE-bind.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001849; PH.
InterPro; IPR000219; RhoGEF.
InterPro; IPR000980; SH2.
InterPro; IPR001980; SH2.
InterPro; IPR00196; SM22_calponin.
Pfam; PF00307; CH; 1.
Pfam; PF00307; CH; 1.
Pfam; PF00307; CH; 1.
                                       Pfam; PF
PRINTS;
PRINTS;
PRINTS;
ProDom;
ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Breast, and Colon carcinoma;

MEDLINE=98371222; pubMed=9705494;

Trenkle T., Welsh J., Jung B., Mathieu-Daude F., McClelland M.;

"Non-stoichiometric reduced complexity probes for cDNA arrays.";

Nucleic Acids Res. 26:3883-3891(1998).

-i-FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,

TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE
STATES OF THOSE GTPASES.

-i-ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;

Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                         Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q9UKW4-2; Sequence=VSP_001820;
-!- SIMILARITY: Contains 1 calponin-homology (CH) domain.
-!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
-!- SIMILARITY: Contains 1 PH domain.
-!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND ALTERNATIVE SP
MEDLINE=99455043; PubMed=10523675;
Movilla N., Bustelo X.R.;
"Biological and regulatory properties
Vav family of oncoproteins.";
Mol. Cell. Biol. 19:7870-7885(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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"FP00130; DAG PB-bind,
pfam; PF00130; DAG PB-bind,
fam; PF00169; PH; 1.
'am; PF00018; SH3; 1.
'm; PF00018; SH3; 1.
'TS; PR00401; SH2DWAIN.
'S; PR00452; SH3DWAIN.
'S; PR00452; SM2ZALPONIN.
'S; PR00452; SM2ZALPONIN.
'PD001527; CH type; 1.
'PD001527; SH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binding domain.
SIMILARITY: Contains 1 SH2 domain.
SIMILARITY: Contains 2 SH3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  i; AF118887; AAD20349.
i; AF118886; AAD20348.
i; AF067817; AAC79695.
i; P29355; ISEM.
HGNC:12659; VAV3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                    605541;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Human)
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AAD20348.1; -.
AAC79695.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                  signal transduction; TAS
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SMART; SM00233; PH;
SMART; SM00325; Rhc
SMART; SM00325; SH2
SMART; SM00326; SH3
PROSITE; PS500479; D
PROSITE; PS50001; D
PROSITE; PS50010; D
PROSITE; PS50010; D
PROSITE; PS50003; P
PROSITE; PS50003; P
PROSITE; PS50003; P
PROSITE; PS50002; S
PROSITE; PS50002; S
PROSITE; PS50002; S
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DOMAIN 192 3

DOMAIN 400 5

DOMAIN 514 5

DOMAIN 672 7

DOMAIN 672 7

DOMAIN 788 8

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CONFLICT
SEQUENCE
                                                                                                              SEQUENCE FROM N.A.

MEDLINE=20179693; Pubmed=10713454;

Trenkle T., McClelland M., Adlkofer K., Welsh J.;

"Major transcript variants of VAV3, a new member of the
guanine nucleotide exchange factors.";

Gene 245:139-149(2000).

Gene 245:139-149(2000).

-i-FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS
TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE
STATES OF THOSE GTPASES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
VAV3_N
                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                              VAV3.
                                                                                                                                                                                                                                                                                                                                                                                                            Vav-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
15-SEP-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9ROCB;
                                                                                                  -
                                      TO A LESSEK DATE TO A LESSEK DATE OF THOSE GTPASES (BI DATE OF THOSE GTPASES)
ALTERNATIVE PRODUCTS:
Alternative splicing; Named isoforms=2;
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; SM00109; CC1; 1.
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; SM00252; SH2; 1.
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CETFGMRKSELFEAFDLFDVRDFGK -> MQLEDCPCRAHL
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tive splicing.
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PROSITE; PS50021; CH; 1.

PROSITE; PS50021; CH; 1.

R PROSITE; PS50081; DAG PE BIND DOM 1; 1.

R PROSITE; PS50001; DH 2; 1.

R PROSITE; PS50001; DH 1; 1.

PROSITE; PS50001; PH DOMAIN; 1.

PROSITE; PS50001; PH DOMAIN; 1.

DR PROSITE; PS50001; SH2; 1.

DR PROSITE; PS50001; SH3; 2.

PROSITE; PS50002; SH3; 2.

PHOTPOI-ester binding; Zinc; SH2 doma Phorbol-ester binding; Zinc; SH2 doma Phorbol-ester binding; Zinc; SH2 doma
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Matches 5
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InterPro; IPR003247; CH type.
InterPro; IPR0032219; DAG PE-bind.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001849; PH.
InterPro; IPR000219; RhoGEF.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001452; SH3.
InterPro; IPR001990; SM22_calponin.
Pfam; PF00307; CH; 1.
Pfam; PF00307; CH; 1.
                                                                                                                                                                                                                                                                                                     ProDom; PD001527; CH_type; 1
ProDom; PD000093; SH2; 1.
ProDom; PD000066; SH3; 1.
SWART; SM00109; C1; 1.
SWART; SM00033; CH; 1.
SWART; SM00233; PH; 1.
SWART; SM00233; PH; 1.
SWART; SM00252; SH2; 1.
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                                                                                                                                                                Guanine-nucleotide
DOMAIN 1
DOMAIN 192
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Pfam; PF000621; RhoGEF; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
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HSSP; P29355; 19
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PHORBOL-ESTER AND DAG BINDING.
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CCC -i- ECCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T "ESTROGEN REGULATION OF THE TUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL CC COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL CC CAMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL CC CAMPLEMENT ENTRY FOR PROTECTION OF THE COMPLEMENT PARTHWAYS. CC THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR INMUNE AGGREGATES. CC FUNCTION. DERIVED FROM PROTEDLYTIC DEGRADATION OF COMPLEMENT C3, CC CIA ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND CC BASOPHILIC LEUKOCYTES.

CC RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE BOND. C3 CONVERTASE ACTIVATES C3 BY CLEAVING THE ALPHA CHAIN, ALPHA
                                        EMBL; X52477; CAA36716.1; ---
EMBL; M99866; AAA40837.1; ALT_SEQ.
PIR; S15764; C3RT.
PDB; 1QOP; 31-JUL-00.
InterPro; IPR0012890, A2M N.
InterPro; IPR000200, Anaphylatoxin.
InterPro; IPR000159; MacrogloblnA2.
InterPro; IPR001134; Netrin_C.
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between the
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Jacobs J.W., Rubin J.S., Hugli T.E., Bogardt R.A.,
Daniels J.S., Daughaday W.H., Bradshaw R.A.;
Purification, characterization, and amino acid secanaphylatoxin (C3a).";
Biochemistry 17:5031-5038(1978).
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"Nucleotide and deduced amino acid sequence of
Nucleic Acids Res. 18:2178-2178(1990).
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Mammalia; Eutheria; Rodentia;
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mm B.S., Ponce-De-Leon H.,
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or [Contains: C3A anaphylatoxin].
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Sciurognathi; Muridae; Murinae; Rattus
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POLG_TBEVS
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Matches
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PO7720; PO7721; Q88475; Q88476; Q88477; Q88478; Q88479; Q88877;
Q88878; Q88879;
01-APR-1988 (Rel. 07, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Genome polyprotein [Contains: Capsid protein C (Core protein); |
Genome polyprotein [Contains: capsid protein E, Nonstru
proteins (SI, NSZA, NSZB, MSYA and NSSB; Protease/helicase
(EC 3.4.21.98) (NS3); RNA-directed RNA polymerase (EC 2.7.7.48)
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SMART; SM00643; C345C; 1.
                                "Nucleotide sequence of the genor of the polyprotein of tick-borne Virology 174:250-263(1990).
                                                                           SEQUENCE FROM N.A.
MEDLINE=90101381; PubMed=2136778;
          SEQUENCE OF 1-1190 FROM N.A.
                               Virology
                                                                   Pletnev A.G.,
                                                                                                                                      Viruses; ssRNA positive-strand
                                                                                                                                                  Tick-borne encephalitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
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MEDLINE=88319988; PubMed=2970626;
                                                                                                             NCBI_TaxID=11087;
                                                                                                                            Flavivirus
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                                Yammshchikov V.F., Blinov v.m.; equence of the genome and complete amino acid equence of tick-borne encephalitis virus.";
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ANAPHYLATOXIN-LIKE.
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N-LINKED (GLCMAC. . .) (PROBABLE)
N-LINKED (GLCMAC. . .) (PROBABLE)
LK -> KL (IN REF. 2).
MW; 2F87CCB143CDD4BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALPHA CHAIN.
C3A ANAPHYLATOXIN
C3B (ALPHA' CHAIN
                                                                                                                                                (strain Sofjin)
                                                                                                                                      viruses,
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Signal; 3D-structure
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                                                                                                                                       DNA stage;
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or send an
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CATALYTIC
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S Lett. 200:317-321(1966).
FUNCTION: THE GMAX'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY ILIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN B. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.

PROTEIN C AND MRNA. NONSTRUCTURAL PROTEINS NS1 PRESENTS TWO ALTERNATIVE CLEAVAGE SITES FOR ITS C-TERMINUS, WHICH MAY DEFINE SOLUBLE OR A MEMBRANE-BOUND FORM OF NS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARI HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCT: NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the con
                prolog; Plavi capsid; 1.
prolog; Plavi glycop C; 1
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prolog; Plavi helicase; 1
prolog; Plavi M; 1.
prolog; Plavi M; 1.
prolog; Plavi NS2A; 1.
prolog; Plavi NS2A; 1.
prolog; Plavi NS2B; 1.
prolog; Plavi NS4B; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001650; Helicase C.
IPR007095; RNA pol DS PS.
IPR007094; RNA pol PSvir.
1003; Flavi capsid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAA27501.1;
CAA27502.1;
CAA27503.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVITY: Hydrolyeis of four peptide bonds in the vipolyprotein, commonly with Asp or Glu in the P6 Cys or Thr in P1 and Ser or Ala in P1.

ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAA30581.1;
CAA27500.1;
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Flavi_glycoprotE;
                                                                                                                                                                                                                                                                                                                                        _capsid; 1.
_glycop_C; 1.
_glycoprot; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Bacteria; Actinobacteria; Mycobacterium.
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STRAIN=CDC 1551 / Oshkosh;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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99 AA; 11535 MW; 276DA391CE96B85B CRC64;
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               2003,
                                                                                                                                  Score 35; DB
Pred. No. 16;
2; Mismatches
                 14:10:47
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Perfect score:
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Maximum Match 100%
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Maximum DB
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1: sp_archea:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	00	7	6	. ഗ	.4.	·	N	, ц	Result No.
40	40	40	40	41	41	41	41	42	42	42	40	52	52	52	52	Score
57.1	57.1	57.1	57.1	58.6	58.6	58.6	58.6	60.0	60.0	60.0	65.7	74.3	74.3	74.3	74.3	Query
285	274	229	229	863	615	441	219	407	401	211	267	1661	349	167	154	Length
ហ	11	16	16	16	16	ഗ	13	IJ	16	16	16	σ	σ	σ	σ	DB
Q18611	Q9D912	Q8FYX0	9AIA8D	Q8DGQ6	Q9СНМ3	Q8T3J9	Q90YC5	Q8SYY7	Q9P9Y5	Q9HYZ4	Q9HTZ5	Q9GKP1	046544	Q9NOM4	Q29289	ID
Q18611 caenorhabdi	Q9d912 mus musculu	Q8fyx0 brucella su	Q8yiy6 brucella me	Q8dgq6 synechococc	Q9chm3 lactococcus	Q8t3j9 drosophila		Q8syy7 drosophila	Q9p9y5 xylella fas	Q9hyz4 pseudomonas	Q9htz5 pseudomonas	Q9gkp1 sus scrofa	O46544 ovis aries	Q9n0m4 cervus nipp	Q29289 sus scrofa	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
38	38	38	38	38	38	38	38	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	40	40	40	40	40
54.3	54.3	54.3	54.3	54.3	54.3	54.3	54.3	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	57.1	57.1	57.1	57.1	57.1
439	432	317	280	269	266	265	250	574	574	572	572	437	410	406	406	387	382	381	322	321	232	197	172	1145	. 541	541	347	338
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Q9NEC1	Q8G4P1	Q90WC0	045477	Q9H4F5	Q8UBV4	Q9NS79	Q9NS78	Q8Y3W3	Q927C5	Q8DXV6	Q8E3H4	Q8MMP7	Q8FU88	Q9JРВ4	P95619	Q8CJT5	Q93EV7	Q8RTQ7	Q91ZB9	Q91ZC0	Q92KX1	Q9HK18	Q8PR28	Q9DBV3	Q8P0P2	Q9A017	Q9VRZ4	Q8PF47
	Q8g4p1 bifidobacte	Q90wc0 agkistrodon	caen	Q9h4f5 homo sapien	Q8ubv4 agrobacteri	homo	homo		Q927c5 listeria in	Q8dxv6 streptococc	Q8e3h4 streptococc		Q8fu88 corynebacte			Q8cjt5 streptomyce	Q93ev7 thermodesul	Q8rtq7 thermodesul	Q91zb9 mus musculu	Q91zc0 mus musculu		Q9hk18 thermoplasm	Q8pr28 xanthomonas		Q8p0p2 streptococc	Q9a017 streptococc	Q9vrz4 drosophila	Q8pf47 xanthomonas

ALIGNMENTS

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RESULT
Q9N0M4
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Q29289
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                                                                                                                                         L Mamm. Genome 7:509-517(1996).

R EMBL; F14640; CAA23173.1; -.

R HSSP; P01024; 1C3D.

InterPro; IPR001599; MacrogloblnA2.

Pfam; PF00207; A2M; 1.

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154 AA; 17440 MW. CONTICE
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Best Local (
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                             TISSUE=Small intestine;

MEDLINE=96327607; PubMed=8672129;

Winteroe A.K., Fredholm M., Davies W.;

"Evaluation and characterization of a porcine small intestine cDNA
library.";
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
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                                                100 VRHRILWESASLL 112
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Similarity 76.9%;
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154 AA; 17440 MW; 6DC7661C1253ED45 CRC64;
                                                                                               Conservative
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                                                                                                          Score 52; DB 6; Length 154; Pred. No. 0.25;
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046544;
01-JUN-1998
01-JUN-1998
01-MAR-2002
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Q9NOM4;
Q9NOM4;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Complement C3 alpha chain (Fragment).
Cervus nippon (Sika deer).
EUKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoide;
Cervidae; Cervinae; Cervus.
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SEQUENCE
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Submitted (MAY-2000) to the EMBL/Ge
EMBL; AF264631; AAF73464.1; -.
HSSP; P01024; IC3D.
InterPro; IPR001599; MacrogloblnA2.
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SEQUENCE
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                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                          J. Immunol. 161:458-466(1998).
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-white alpine; TISSUE-Liver; MEDLINE=98309471; PubMed=9647256; Hein W.R., Dudler L., Marston W.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ovis aries (Sheep).
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Mammalia; Eutheria;
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Pro; IPR001599; MacrogloblnA2
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(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
component C3 (Fragment).
                                                                                 Conservative
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Pred. No. 0.
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Q9HTZ5;
01-MAR-2001
01-MAR-2001
01-JUN-2002
SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed=10984043;

MEDLINE-20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9GKP1;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9GKP1
                                                                                                                                                                                                                                                                                         Hypothetical PA5194.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAR-2003
                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Polymorphic sites in exon 15 and Anim. Genet. 32:46-47(2001). EMBL; AF154933; AAG40565.1; -.
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                                                                                                                                                                                                       NCBI_TaxID=287;
                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000020;
InterPro; IPR001840;
InterPro; IPR001599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro; IPR002890; A2M_N.
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3 (TrembLrel. )
7 (Tremblrel. )
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1 (TrEMBLrel. 21, )
2 (TrEMBLrel. 21, )
31 protein PA5194.
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                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=11419349;
ay S., Ponsuksili
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Cetartiodactyla; Suina; Suidae;
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Anaphylatoxn.
MacrogloblnA2.
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16,
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Last annotation updat
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Last sequence update)
Last annotation updat
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Sus.
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RESULT
Q9P9YS
ID Q9
AC Q9
AC Q9
DT 01
DT 01
DT 01
DT 4y
GN XF
OS XY
OC Ba
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Best L
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                                               01-OCT-2000
01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-APCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., La Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yu Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                  Q9P9Y5;
                                                                                                                                                                                                                                                                       InterPro; IPR006145; PseudoU_synth.
InterPro; IPR006224; PSI_RLU;
Pfam; PF00849; PseudoU_synth 2; 1.
ProDom; PD001819; PSI_RLU; 1.
PROSITE; PS01129; PSI_RLU; 1.
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InterPro; IPR000236; PA
Pfam; PF01569; PAP2; 1.-
Hypothetical protein; Complete
SEQUENCE 267 AA; 30527 MW;
                       Hypothetical XF2735.
                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406:959-964(2000).
BEBLI, AB004747; AAG06634.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence opportunistic pathogen."; Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
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01-MAR-2003
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 Bacteria; Proteobacteria;
             Xylella fastidiosa
                                                                                                                                                                                                                                                      SEQUENCE
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211 AA;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                 (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation updat
protein Xf2735.
                                                                                                                                                                                                     Conservative
                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                     24338 MW;
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46.2%;
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Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gammaproteobacteria; Pseudomonadales;
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E
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Pred. No.
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Pred. No. 4.9;
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57CD9D2319B6AD7D CRC64;
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n S., Yuan Y.,
K., Lim R.M.,
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RESULT
Q8SYY7
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RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Marques M.V., Marcins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Manck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA Quaggio R.B., Roberto P.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA da Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
"The genome sequence of the plant pathogen Xylella fastidiosa.";
Marure 406:151-159(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                 Stapleton M., Brokstein P., Hong I., Agbayani A., Carlson J., Chawez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bave J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit f
Eukaryota; Metazoa; Arthropoda
Neoptera; Endopteryoota; Diptera
Ephydroidea; Drosophilidae; Dros
                                                                                                                                                                                                                                                                                                                         RE27547p (CG1859
                                                                                                                                                                                                                                                                                                                                                                                                      Q8SYY7; Q9V4I4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; SEQUENCE 401 AA; 4
SEQUENCE FROM N.A.
                                    Submitted
                                                     Celniker S.
                                                                                                                                                            STRAIN=Berkeley;
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                CG1859
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                                  (DEC-2001) to
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                                                                                                                                                                                                                                                                                                                               protein).
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                                  the
                                                                                                                                                                                                                                                                                                                                              23,
                                                                                                                                                                                                                                   ropoda; Hexapoda; Insecta; Pterygota;
   Diptera; Brachycera; Muscomorpha;
ae; Drosophila.
                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Pred. No. 37;
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RA Abril J.F., Agbayani A., An H.-J., Naturews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadeu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.C., Evragelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
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RA Merkulov G., Milshina N. V., Mobarry C., Morris J., Moshrefi A.,
RA Rainert K., Remington K.A., Nixon K., Nusskern D., M., Nelson D.L.,
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RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
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Celniker
Adams M.D., Celniker Submitted (MAR-2000) [6]
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EMBL/GenBank/DDBJ
                            G.M., Vent
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Best Local
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Q8T3J9, Q9VLX7;
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-OCT-2002 (TrEMBLrel. 2
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SEQUENCE FROM N.A.
MEDLINE=21412237; PubMed=11520665;
MEDLINE=21412237; PubMed=11520665;
Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;
"Identification of ephrin-A3 and novel genes specific to the midbrain-
"Identification of ephrin-A3 and novel genes specific to the midbrain-
"Identification of ephrin-A3 and novel genes specific to the midbrain-
"Identification of ephrin-Based differential display.";
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01-DEC-2001
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1: SIMILARITY: BELONGS TO THE
EMBL; AY071238; AAL48860.1; -
EMBL; AB003842; AAF59286.2; -
FlyBase; FBgn0033147; CG1859.
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PROSITE;
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Pfam; PF00079; serpin; 1.

PROSITE; PS00284; SERPIN; 1.

Protease inhibitor; Serine protease inhibitor; Serpin.

Protease inhibitor; Serine protease inhibitor; Serpin.

PROTENCE 407 AA; 44863 MW; 5D2A46A75CB6DD78 CRC64;
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Submitted (SEP-2002)
-!- SIMILARITY: BELOW
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EMBL, AB051678; BAB55891.; --
ZFIN; ZDB-GENE-011108-1; efna3.
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Brachydanio rerio (Zebrafish) (Danio rerio).

Bukatyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota, Metazoa; Chordata; Teleostei; Ostariophysi; Cypriniformes;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001799; Ephrin. Pfam; PF00812; Ephrin; 1. PRINTS; PR01347; EPHRIN.
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NCBI TaxID=
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Ephydroidea;

Drosophilidae; Drosophila

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RA Adams C.J., Fouriers S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Hilt R.A., Sahburner M., Henderson S.N., RA Adams M.D., Celniker S.E., Hilt R.A., Sabburner M., Henderson S.N., RA Brandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D., RA Ballew R.M., Basu A., Baster E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Bartis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport B.D., Davies P., RA Borkis K.C., Busam D.A., Danj Z., Mays A.D., Dew I., Dietz S.M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Lin X., Mattei B., McIntosh T.C., McLeod M.P., Kenison D.A., Ketchum K.A., RA Halshin D., Houston K.A., Howland T.J., Wei M.-H., Diegwam C., RA McKulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Nelson D.L., Raft C., Kravitz S., Kulp D. Lai Z., Liang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., Moshrefi A., Ra Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Ra Sylrakas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wassaman D.A., Weinson M., Skupski M.P., Smith T., Ra Sylrakas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wassaman D.A., Weinston M., Shang S., Zhao Q., Zheng L., Zhao Q., Zheng L., Zhao G., Zheng L., Zhao D., Zheng L., Zhao G., Zheng L., Z
                                                             RT Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

A Carlson J., An H., Baldwin D., Banzon J., Beson K.Y., Busam D.A.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson K., Dorsett V., Doup L.B., Doyle C., Dresnek D., Farfan D.,

A Perriera S., Frise E., Galle R.F., Garly N.S., George R.A.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

A Pacleb J., Paragas V., Park S., Patel S., Feiffer D.,

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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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SMART; S
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Genome Res. 11.731-753 (2001).
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InterPro; IPR003593; AAA ATPase.
InterPro; IPR001140; ABC TM transpt.
InterPro; IPR003439; ABC_transporter.
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Bolotin A., Wincker P., Mauger S., Jaillon O.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
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C STRAIN=16M / ATCC 23456 / Biotype 1;

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RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los RA DelVecchio V.G., Kapatral V., Redkar R.J., Lykidis A., Reznik G., RA Ivanova N., Anderson I., D'Souza M., Bernal A., Mazur M., Goltsmar RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsmar RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., RA Haselkorn R., Kyrpides N., O'verbeek R.;

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EMBL, AP005376; BAC09811.1; -.
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Brucellaceae; Brucella.
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
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A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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STRAIN=C57BL/6J; TISSUE=Pancreas;
MEDLINE=21085660; PubMed=11217851;
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Mammalia; Eutheria;
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Paulsen I.T., Seshadri R., Nelson K.E.,
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P., Ring B., Ringwatu H., Sato K., Schoenbach C.,
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Rodentia;
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58.3%;
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Last sequence update)
Last annotation updat
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Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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98A1769A370F52CA CRC64;
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   orch K.-F., Wilming L.,
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Q8PF47
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Best Local Similarity
Tatches 6; Conserv
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Q8PF47;
Q8PF47;
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q18611;
Q18611;
01-NOV-1996
01-OCT-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                      "Direct Submission.";
Submitted (JUN-2001) to the
EMBL; U41030; AAA82366.2; -.
WormPep; C44Cl.1; CE27851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bradshaw H., Stellyes L., "The sequence of C. elegans Submitted (DEC-1995) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical C44C1.1.
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Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 285 AA; 32140 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
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EMBL; AK007461; BAB25050.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C. investigating biology. The C. elega Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        None;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki
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                                                                                                                                                      THVLHWES 218
                                                                                                                                                                                             THRIHWES 9
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(TTEMBLrel. 18, Last sequence update)
(TTEMBLrel. 23, Last annotation update)
1 32.1 kDa protein.
                                                                                                                                                                                                                                        Conservative
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(TrEMBLrel. 22,
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                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nematoda; Chromadorea; Rhabditida; Rhabditoidea; inae; Caenorhabditis.
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85.7%;
                                                                                                                                                                                                                                                           57.1%;
75.0%;
                                                                                                                                                                                                                                      Score 40; DB
Pred. No. 57;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
  Created
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EMBL/GenBank/DDBJ databases
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Pred. No.
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                                           PRT;
                                                                                                                                                                                                                                                                                                                             3119FDD3CB1212EE CRC64;
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                                                                                                                                                                                                                                                                               Length 285;
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RESULT 18
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CSTRAIN-306 / ATCC 13002 / XV 101;

X MEDLINB-22022145; PubMed=12024217;

XX MEDLINB-22022145; PubMed=12024217;

XX MEDLINB-22022145; PubMed=12024217;

XX MEDLINB-22022145; PubMed=12024217;

XX MEDLINB-22022145; PubMed=12024217;

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Best Local :
STRAINE Berkeley:
STRAINE 20196006; PubMed=10731132;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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Belson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Besson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P.,
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EMBL; AE012064; AAM38974.1; -..
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InterPro; IPR001005; Myb DNA_binding.
PROSITE; BS00334; MYB 2; 1.
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RA Dodson K., Dough L.E., Downes M.D., Dew I., Dietz S.M.,
RA Dodson K., Dough L.E., Downes M.D., Dunkov B.C., Carrier B.C., Carrier B.C., Gong P.N., M.G., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pecleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pecleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Peri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
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Stapleton M., Brok
Champe M., Chavez
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SEQUENCE FROM N.A.
STRALN=MGAS8232 / Serotype M18;
MEDLINE=2192759; PubMed=11917108;
MEDLINE=2192759; PubMed=11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chau Smoot J.C., Barbian K.D., Ricklefs S.M., Porcella S.F., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=SF370 / ATCC 700294 / Serotype M1;

MEDLINE=21192684; PubMed=11296296;

Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G

Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S.,

Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., Whi

Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

"Complete genome sequence of an M1 strain of Streptococcus

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

EMBL; AB006544; AAX33880.1; -
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Q9A017;
                                                                                                                                                                                                                                                       Hypothetical
SPYM18_1275.
                                                                                                                                                                                                            Streptococcus pyogenes (serotype M18). Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006528; PhageSPP1_gp7.
TIGRPAMS; TIGR01641; phageSPP1_gp7; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 541 AA; 62314 MW; 5F3DF575EF705BC6
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                                                                                                                                                          NCBI_TaxID=186103;
                                                                                                                                                                                         Streptococcus
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AY113342; AAM29347.1; -.
ise; FBgn0035719; CG14821.
INCE 347 AA; 38140 MW;
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(Tremblrel. 22, I
(Tremblrel. 23, L
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enton S., Lai H.S., Lin
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Fruuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Buruki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Hayashiyaki V., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Query Match
Best Local Similarity
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Q9DBV3;
01-JUN-2001
01-JUN-2001
01-MAR-2003
                                                                                    PROSITE; PS00202; RÜBREDOXIN; 1.
ATP-binding; Helicase; Hydrolase.
SEQUENCE 1145 AA; 128624 MW;
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SMART; SM00487; DEXDc; 1.
SMART; SM00490; HELICC; 1
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InterPro; IPR006528; PhageSPP1 gp7.
TIGRRAMs; TIGR01641; phageSPP1 gp7; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 541 AA; 62419 MW; F6A0DD87C6939473 CRC64;
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EMBL; AE010050;
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=21085660; PubMed=11217851;
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); IPR001410; DEAD.

); IPR001650; Helicase C.

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); IPR007087; Znf C2H2.
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Pred. No. 1.1e+02;
   Score 40; DB 11;
Pred. No. 2.4e+02;
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                                                                                          A7E1CDED77FED4C0 CRC64;
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SEQUENCE FROM N.A.

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01-MAR-2001
01-MAR-2001
01-MAR-2003
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01-OCT-2002
01-OCT-2002
                                                                                                                                                                TA0790.
Thermoplasma acidophilum.
Archaea; Euryarchaeota; Thermoplasmata;
Archaea; Thermoplasma.
STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
Ruepp A., Grami W., Santos-Martinez M.-L.,
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EMBL; AE011637; AAM35030.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xanthomonadaceae;
NCBI_TaxID=92829;
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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                                                                                             SEQUENCE FROM N.A.
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5; Conserv
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
s III related protein.
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Pred. No. 50;
4; Mismatches
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5A62A85829AD9718 CRC64;
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      Koretke K.K.,
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Best Local S
Matches 7
Q91ZC0
Q91ZC0;
01-DEC-2001
01-DEC-2001
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat.
Hypothetical protein R03328.
R03328 OR SMC04094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Boutry M., Cadleu E., Dreano S., Gloux S. Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizoblum meliloti strain 1021."; Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
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SEQUENCE
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Nature 407:508-513(2000).
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01-DEC-2001
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HSSP; P20625; 2ABK.
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Bacteria; Proteobacteria; Alphaproteobacteria;
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Pfam; PF00730; HhH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
SMART; SM00525; FES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical SEQUENCE 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobiaceae; Sinorhizobium.
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InterPro; IPR003651; Fes_bind.
InterPro; IPR000445; HhH.
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197 AA; 22753 MW;
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; Pred. No. 68;
1; Mismatches
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Pfam; PF00001; 7tm 1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1 1;
PROSITE; PS50262; G_PROTEIN_RECEP_F12;
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Cell 106:619-632 (2001).
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_2;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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"A Diverse Family of GPCRs Expressed
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                                                                                                                                                                     Score 39;
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RESULT 27 Q8RTQ7 ID Q8RTQ

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RESULT
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01-MAR-2003
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Q93EV7;
01-DEC-2001
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Bacteria; Thermodesulfobacteriales;
Thermodesulfobacteriaceae; Thermodesulfobacterium.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Dissimilatory sulfite reductase alpha subunit (Fragment).
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Submitted (MAY-2000) to the EMBL/GE
EMBL; AF271771; AAL78311.1; -
InterPro; IPR006067; Nir Sir 4Fe4S
Pfam; PF01077; NIR SIR; I.
NON_TER 1
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MEDLINE=21450829; PubMed=11567003;
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Bacteria; Thermodesulfobacteria; Thermodesulfobacteriales;
Thermodesulfobacteriaceae; Thermodesulfobacterium.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Dissimilatory sulfite reductase alpha subunit (Fragment).
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Abicht H., Blackall L.L., Stahl D.A., Wagner M.;
"Multiple Lateral Transfers of Dissimilatory Sulfite Reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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01-JUN-2002
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    (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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50.0%;
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Pred. No. 1.1e+02;
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Pred. No. 1.1e+02
4; Mismatches (
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Nature 417:141-147(2002).
EMBL; A1939120; CAD55486.1; -
Hypothetical protein; Complet
SEQUENCE 387 AA; 44420 MW;
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P95619;
01-MAY-1997
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MEDLINE=21996410; PubMed=12000953;
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Streptomyces coelicolor.
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U73944; AAC44799.1; -.
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roteobacteria; Betaproteobacteria; Burkholderiales;
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01-MAR-2003 (TrEMBLrel.
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Corynebacterineae; Corynek
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Biochemistry 38:15238-15244(1999).
EMBL; AB034704; BAA94047.1; -.
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Parot P., Vermeglio A.;
"Dark aerobic growth conditions induce t
midpoint potential cytochrome c8 in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20031519; PubMed=10563807; Menin L., Yoshida M., Jaquinod M.,
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on photosynthesis), pp
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Nagashima K.V., Matsuura K., Ohyama S., Shimada K.;
"Primary structure and transcription of genes encoding B870
photosynthetic reaction center apoproteins from Rubrivivax
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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  N.A.
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STRAIN=NEM316 / Serotype III;
STRAINE=22242508; PubMed=12354221;
MEDLINE=22242508; PubMed=12354221;
MEDLINE=22242508; PubMed=12354221;
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01-MAR-2003
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SEQUENCE
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Methionyl-tRNA synthetase beta subunit. 6/101.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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Ikeo K., Suzuki M., Ma
Usuda Y., Sugimoto S.;
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Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi
                                                                                                                                  NCBI_TaxID=216495;
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InterPro; IPR002616; tRNA_ribo_trans.
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Listeria innocua.
Bacteria; Firmicutes; B
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MEDLINE=22222988; PubMed=12200547;
Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Carby H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M. Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G., "Fraser C.M.,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8DXV6;
Q8DXV6;
01-MAR-2003
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01-MAR-2003
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Hypothetical protein; Complete proteome.
SEQUENCE 572 AA; 64458 MW; 9CB68B07FA063F9E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding; companies 572 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence and comparative genomic analysis of emerging human pathogen, serotype V Streptococcus agalactiae.' Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=2603 V/R /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=216466;
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5; Conser
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1 (TrEMBLrel.
3 (TrEMBLrel.
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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72 AA; 64423 MW;
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83.3%;
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83.3%;
  Bacillales; Listeriaceae; Listeria.
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19,
23,
                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                                 Created)
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Pred. No. 1.8e+02;
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Pred. No. 1.8e+02;
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RESULT 37
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Best Local S
Matches 5
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
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Q8Y3W3;
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,
Domann B., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurabkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
                                                                                                              Science 294:849-852(2001).
EMBL; AL591984; CAD00929.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listeria monocytogenes.
Bacteria; Firmicutes; E
NCBI_TaxID=1639;
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01-MAR-2003
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Pfam; PF00005; ABC tran; 1.
ProDom; PD000006; ABC transport
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STRAIN=CLIP 11262 / Serovar 6a;
PubMed=11679669;
                                                                                  ListiList; LMO02716;
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SMART; SM00382; AAA;
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EMBL; AL596173; CAC98090.1; -.
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                                                        InterPro;
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        IPR003593;
IPR001140;
IPR003439;
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; ABC_TM_transpt.
; ABC_transporter.
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AAA_ATPase.
ABC_TM_transpt.
ABC_transporter.
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Last annotation update)
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Pred. No. 1.8e+02;
1; Mismatches 0
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RESULT 39
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Best Local
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SMART; SM00382; AAA;
Complete proteome.
SEQUENCE 574 AA; 6:
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Q9NS79;
01-OCT-2000
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SEQUENCE FROM N.A.

TISSUE-Spinal cord;
Aerbajinai W., Arahata K., Tsukahara T.;
"Increased expression level of a novel alternative splication in motor neuron diseases.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases EMBL, AB037701; BAB03508.1; -.

InterPro; IPR007022; SIP1.
Pfam; PF04938; SIP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUB-Spinal cord;
Aerbajinai W., Arahata K., Tsukal
Merbajinai W., Arahata K., Tsukal
"Increased expression level of a
SIP1 in motor neuron diseases.";
Submitted (JAN-2000) to the EMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SMN interacting protein 1-gamma.
                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                     SMN interacting
                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007022; SIP1.
Pfam; PF04938; SIP1; 1.
SEQUENCE 250 AA; 28155
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Mammalia; Eutheria;
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                                                                                                                                                 Homo
                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                sapiens (Human)
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                                                                                                                                                                                                                             PRELIMINARY;
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Primates;
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83.3%;
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l of a novel alternative splicing variant of
                                                                                                                                                                                 Last sequence update)
Last annotation updat
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1; Mismatches
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L; Mismatches
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1.1e+02
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Search completed: Job time : 95 secs

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Best Local S
Matches 6
                                                            Query Match
Best Local S
Matches 7
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Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon
Raymond S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
Nester E.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat.)
Hypothetical proteoin Atu2746.
ATU2746 OR AGR C 4981.
AGROBACTERIAL TROUBLES (Strain C58 / ATCC 3397)
Bacteria, Proteobacteria, Alphaproteobacteria, Rh Rhizobiaceae, Rhizobium.
MCBI TaxID=176299;
                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=21608551; PubMed=11743194;

MEDLINE=21608551; PubMed=11743194;

MEDLINE=21608551; PubMed=11743194;

MILLER N., Blanchard M.,

Quodin B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin :

Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B

Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,

Cielo C., Slater S.;

"Genome sequence of the plant pathogen and biotechnology agent

Agrobacterium tumefaciens CSB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8UBV4;
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                                                                                                                            Hypothetical protein; Complete proteome.
SEQUENCE 266 AA; 29620 MW; 40B98CC626C43B27 CRC64;
                                                                                                                                                        EMBL; AE009222; AAL43727.1; ALT_INIT.
EMBL; AE008188; AAK88461.1; -.
                                                                                                                                                                                          Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome
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180
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Alphaproteobacteria; Rhizobiales;
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Pred. No.
                                                            Score 38; DB 16;
Pred. No. 1.2e+02;
L; Mismatches 4
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